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Result
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Listing first 45 summaries
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10756.968 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AY725471 Synthetic
AX111695 Sequence
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71.2	71.4	71.4	71.4	71.4	71.4	71.5	71.5	71.5	71.6	71.6	71.6	71.6	71.6	71.9	71.9	72.1	72.2	72.2	72.6	72.7	72.7	72.8	73.1	73.2	74.1
729	2213	786	717	810	810	723	726	726	276248	138860	110000	61804	61582	720	719	738	1797	2364	732	726	726	726	894	789	717
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AY171038	AC087118	AF279665	AF025535	CQ876881	CQ873224	AY307933	AR063196	A46596	AC087561	AC055703	AC074222_3	AC027647_3	RN499P20	AR117135	AR100151	AY635846	I84705	E13412	E13410	AR063195	A46594	A46598	AR316970	AF488378	AF367377
AY171038 Synthetic	AC087118 Mus muscu	AF279665 Synthetic	AF025535 Mus muscu	CQ876881 Sequence	CQ873224 Sequence	AY307933 Synthetic	AR063196 Sequence	A46596 Sequence 27	AC087561 Mus muscu	AC055703 Mus muscu	Continuation (4 of	Continuation (4 of	AL603720 Rattus no	AR117135 Sequence	AR100151 Sequence	AY635846 Synthetic	I84705 Sequence 2	E13412 cDNA encodi	E13410 cDNA encodi	AR063195 Sequence	A46594 Sequence 25	A46598 Sequence 29	AR316970 Sequence	AF488378 Mus muscu	AF367377 Synthetic

ALIGNMENTS

RESULT 1

Db 1	Ωγ 1	Db 1	Qy 1	Db	Sy.	В	Ş	Query Match Best Local Matches 71	ORIGIN	source	FEATURES	JOURNAL		TITLE	AUTHORS	REFERENCE	ORGANIZAN	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AR231454
181 AAGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTAC 240	181 AAGCAGAAGTTCAAGGGCAAGGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTAC 240	121 CATGGAAAGAGCCTTGAGTGGATTGGAGGTATTAATCCTAACAATGGTGGTACTAACTA	121 CATGGAAAGAGCCTTGAGTGGATTGGAGGTATTAATCCTAACAATGGTGGTACTAACTA	61 TCCTGCAAGACTTCTGGANACAAATTCACTGAATACACCATGCACTGGGTGAAGCAGAGC 120	61 TCCTGCAAGACTTCTGGANACAAATTCACTGAATACACCATGCACTGGGTGAAGCAGAGC 120	1 CAGGTGAAACTGCAGCAGTCAGGACCTGAACTGGTGNAGCCTGGGGCTTCAGTGAAGATA 60	1 CAGGTGAAACTGCAGCAGTCAGGACCTGAACTGGTGNAGCCTGGGGCTTCAGTGAAGATA 60	<pre>/ Match 99.7%; Score 715; DB 6; Length 717; Local Similarity 100.0%; Pred. No. 4e-211; les 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	/mol_type="genomic DNA"		Location/Qual	Patent: US 6451995-A 1 17-SEP-2002;	anti-ganglioside GD2 antibodies, cells expressing same and related	5.	eung, N.	1 (bases 1 to 717)		Unknown.	•	AR231454.1 GI:27272556		1 from patent US 6451995.	AR231454 717 bp DNA linear PAT 20-DEC-2002	

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JOURNAL
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Sequence 3 f
AR231456
AR231456.1
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                                                                                                                                                                                                                                                                                                                               Unknown
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                                                                                                                 CAGGTGAAACTGCAGCAGTCAGGACCTGAACTGGTGNAGCCTGGGGCTTCAGTGAAGATA
                               TCCTGCAAGACTTCTGGANACAAATTCACTGAATACACCATGCACTGGGTGAAGCAGAGC
 AAGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTAC
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ilarity 100.0%;
Conservative
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Location/Qualifiers
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                                                                                                                                                                                                             /organism="unknown"
/mol_type="genomic
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Pred. No. 4.1e-211;
0; Mismatches 0;
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Sequence
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Solomon,B. and Frenkel,D.
Filamentous bacteriophage displaying
Patent: US 6703015-A 5 09-MAR-2004;
Location/Qualifiers
1. .717
                                                                                                                                                                                                                                                                                                       Unknown.
                                                                                                                                                                                                                                                                                              Unclassified.
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AAGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTAC
                               TCCTGCAAGGGTTCTGGCTACACATTCACTGATTATGCTATGCACTGGGTGAAGCAGAGT
                                                                                     TCCTGCAAGACTTCTGGANACAAATTCACTGAATACACCATGCACTGGGTGAAGCAGAGC
                                                                                                                CAGGTGAAACTGCAGCAGTCAGGACCTGAACTGGTGNAGCCTGGGGCTTCAGTGAAGATA
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Pred. No. 3.2e-173;
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Submitted (24-NOV-1997) LMB, NCI, 37
4B20, Bethesda, MD 20892-4255, USA
Location/Qualifiers
                                                                                                                                                                                    2 (bases 1 to 723)
Chowdhury, P.S.
                                                                                                                                                                                                                             1 (bases 1 to 723)
Chowdhury, P.S., Viner, J.L., Beers, R. and Pastan, I.
Isolation of a high-affinity stable single-chain Fv specific for mesothelin from DNA-immunized mice by phage display and construction of a recombinant immunotoxin with anti-tumor activity proc. Natl. Acad. Sci. U.S.A. 95 (2), 669-674 (1998)
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                                                                                 /mol_type="mRNA"
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/db_xref=""-"
                                                      mice
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Eutheria; Rodentia;
/codon_gtart=1
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mice immunized with DNA"
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          synthetic construct
other sequences; artificial sequences.
1 (Dases 1 to 735)
Terrada,E., Kerschbaumer,R.J., Giunta,
                                                       synthetic
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SSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPGRFSGGSGNSYSLTISSVEAEDDA

TYYCQQWSGYPLTFGAGTKLEIK"
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Similarity ATGGAGCTCCGCAGCCTGACATCTGAGGATTCTGCAGTCTATTACTGTGCAAGAGATACT CAGGTGAAACTGCAGCAGTCAGGACCTGAACTGGTGNAGCCTGGGGCTTCAGTGAAGATA AAGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTAC CATGGAAAGAGCCTTGAGTGGATTGGACTTATTACTCCTTACAATGGTGCTTCTAGCTAC TCCTGCAAGACTTCTGGANACAAATTCACTGAATACACCATGCACTGGGTGAAGCAGAGC CAGGTACAACTGCAGCAGTCTGGGCCTGAGCTGGAGAAGCCTTGGCGCTTCAGTGAAGATA GGGACCTCTTATTCTCTCACAATCAGCAGCATGGAGGCTGTAGATGCTGCCACTTATTAC TACGACGGGAGGGGTTTTGACTACTGGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGT ACGGTCCCG-----TTTGCTTACTGGGTCCAAGGGACCACGGTCACCGTCTCCTCAGGT TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACACCATGAACTGGGTGAAGCAGAGC TGCCATCAGCGGAGTAGTTACCCGCTCACGTTCGGTGCTGGGACACAGTTGGAAATAAAA 714 ATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTTCGGCTTCAGTGGCAGTGGGTCT TCAAGTATAAGTTACATGCACTGGTACCAGCAGAAGCCTGTCACCTCCCCCAAAAGATGG **AACCAGAAGTTCAGGGGCAAGGCCACATTAACTGTAGACAAGTCATCCAGCACAGCCTAC** TGCCAGCAGTGGAGTGGTTACCCTCTCACGTTCGGTGCTGGGACAAAGTTGGAAATAAAA GGAAACTCTTACTCTCACAATCAGCAGCGTGGAGGCTGAAGATGATGCAACTTATTAC ATTTATGACACATCCAAACTGGCTTCTGGAGTCCCAGGTCGCTTCAGTGGCAGTGGGTCT TCAAGTGTAAGTTACATGCACTGGTACCAGCAGAAGTCAGGCACCTCCCCAAAAGATGG Conservative 82.3**%**; 89.7**%**; Score 590.4; Pred. No. 2.8e 0; Mismatches <u>..</u> B 10; 2.8e-172; les 68; Indels Length 6 Gaps 300 663 654 603 594 543 534 483 474 423 414 363 354 303 243 240 183 180 123 120 63

735 bp mRNA linear acconstruct single chain antibody 3CA5 mRNA,

SYN 13-JUL-2000 partial cds.

GI:9081896

Giunta, G.,

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                    TATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTATAAGTTACATGCACTGGTACCAGGAGAAGCCTGTCACCTCCCCCGAAAAGATGGATT
                                                                                                                                                                  CCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGGCAGCTCA
                                                                                                                                                                                                                                                                                GATCACTACTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGA
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TATCTCACATCCAACCTGGCTTCTGGAGTCCCTGAACGCTTCAGTGGCAGTGGGTCTGGG
                                                                       AGTGTAAGTTACATGTACTGGTACCAGCAGAAGCCAGGATCCTCCCCCCAAACCCTGGATT
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SSSVSYMYWQQKFGSSPKPHYLTISNIASGVPERFSGSGSGTSYSLTISSMEAEDAA
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/db_xref="taxon:32630"
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/note="derived from variable regions of heavy and light
chains of an antibody isolated from hybridoma cells of Mus
musculus (BALB/c strain)"
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Zhao, B. and Xu, C.
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                                                                                      AATGAGAAATTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTAC
                                                                                                                     AAGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTAC
                                                                                                                                                                                                CCTGGACAGGGACTTGAGTGGATTGGATGGATTTATCCTGGAGATGGTAGTACTAAGTAC
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/translation="MOVELQESGP
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                                                        CTTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGTTGAAGCAGAGGC
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="scFv kodierende Sequenz"
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Downregulation of ca 125 tumor antigen
Patent: WO 03076465-A 1 18-SEP-2003;
Universite de Sharbrooke (CA)
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/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noEe="VH-linker-VL portion of
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Pred. No. 1.7e-161;
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                                                                                                                                                                                                                                                                            Beninati,C., Arseni,S., Mancuso,G., Magliani,W., Conwidiri,A., Biondo,C., Polonelli,L. and Teti,G.
Protective immunization against group B meningococci anti-iddotypic mimics of the capsular polysaccharide
J. Immunol. 172 (4), 2461-2468 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                              723 bp synthetic construct anti-idiotypic fragment mRNA, partial cds. AY374128
                                                                                                                                                                                                     Beninati, C., Arseni, S., Mancuso, G., Magliani, W., Midiri, A., Biondo, C., Polonelli, L. and Teti, G. Direct Submission
                                                                                                                                                                     Submitted (26-AUG-2003) Pathology and Experimental Microbiology, University of Messina, Via C. Valeria, 1 (Policlinico), Messina,
                                                                                                                                                                                                                                                                                                                                                                                          synthetic construct
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/note="binds to anti-meningococcal Seam 3 monoclonal antibody; mimics immunogenic features of group B meningoccoccal polysaccharide"
                                                         /mol_type="mRNA"
/isolation_source="Mus
/db_xref="taxon:32630"
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/transl_table=11
/product="anti-idiotypic
fragment"
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/db_xref="GI:34979268"
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Pred. No. 9.5e-160;
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Best Local Similarity 85.2%;
Matches 610; Conservative
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Continuous in vitro evolution
Patent: JP 2002515224-A 4 28-MAY-2002;
DIATECH PTY LTD

OS Homo sapiens (human)
PD 2002515224-A/4
PD 28-MAY-2002
PF 07-MAY-1999 JP 2000548452
PF 08-MAY-1998 AU
PP 3445
PI GREGORY COIA, PETER JOHN HUDSON, PETER ILIADES,R
PI TRVING
PC C12N15/09,C12N15/01,C12P21/02,C12N15/00,C12N15
Description of Sequence:Antihepatitis surface antig
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JP 2002515224-A/4.
Homo sapiens (human)
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         TAAGTTACATGCACTGGTACCAGCAGAAGAGCCTGTCACCTCCCCAAAAGATGGATTTATG
                                                      CAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGGCAGCTCAAGTA 481
                                                                                    GTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATTGTGCTGACCCAATCTCCAG
                                                                                               ACTGGTCCTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGAGGCG
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C12N15/09,C12N15/01,C12P21/02,C12N15/00,C12N15/00
c1ption of Sequence:Antihepatitis surface antigen
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y 2002515224-A/4
28-MAY-2002
07-MAY-1999 y 2000548452
08-MAY-1998 AU PP 3445
CREGORY COIA, PETER JOHN HUDSON, PETER ILIADES, ROBERT
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 6.2e-159;
0; Mismatches 106;
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TCAGGTACGTGCACTGGTACCAACAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATG
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1 (bases 1 to 807)
Coia,G., Hudson,P.J., Iliades,P. and
Continuous in vitro evolution
Patent: US 6562622-A 4 13-MAY-2003;
Location/Qualifiers
TAAGTTACATGCACTGGTACCAGCAGAAGCCTGTCACCTCCCCCAAAAGATGGATTTATG
                                                                   CAATCATGTCTGCATCTCCCAGGGGAGAAGGTCACCATGACCTGCAGTGGCAGCTCAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGCAAGACTTCTGGANACAAATTCACTGAATACACCATGCACTGGGTGAAGCAGAGCC
                                                                                                                                               ACTGGTCCTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGAGGCG
                                                                                                                                                                                                                       CGGTCCCGTTTGCTTACTGGGTCCAAGGGACCACCGTCACCGTCTCCCTCAGGTGGAGGCG
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                                                                                                                          GTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATTGTGCTGACCCAATCTCCAG
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                                                CAATCATGTTCGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAACTCACGTG
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nilarity 85.2%;
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Pred. No. 6.2e-159;
0; Mismatches 106;
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1 (bases 1 to 1815)
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Direct Submission
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encephalitis virus
Hybridoma 19 (1), 1-13 (2000)
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EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDXAVEWESNGQPENNYKTTPPVLDSDG
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/db xref="taxon:32630"
/cell line="hybridoma expressing a monoclonal antibody
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                    TACTGCCATCAGCGGAGTAGTTACCCGCTCACGTTCGGTGCTGGGGACACAGTTGGAAATA
                                                                               TCTGGGACCTCTTATTCTCTCACAATCAGCAGCATGGAGGCTGAAGATGCTGCCACTTAT
                                                                                                    TCTGGGACCTCTTATTCTCTCACAATCAGCAGCATGGAGGCTGTAGATGCTGCCACTTAT
                                                                                                                                                               TGGATTTATGGCACATCCAACCTGGCTTCTGGAGTCCCTGTTCGCTTCAGTGGCAGTGGA
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87.2%;
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Pred. No. 2e-158;
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nilarity 85.8%;
Conservative
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HEIKE (CA); BOSSLET KLAUS (U
Location/Qualifiers
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/mol_type="unassigned D)
/db_xref="taxon:10095"
/tissue_type="MILZ"
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                                        from
                            GI:45112092
artificial sequences
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Pred. No. 5.2e-157;
0; Mismatches 98;
                                         811 bp DNA
WO2004007550.
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Beste,G.
Mcam inhibitors
Patent: WO 20040
Xerion Pharmaceu
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Similarity 86.2%;
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Pharmaceuticals GmbH
Location/Qualifiers
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/mol_type="unassigned I
/db_xref="taxon:32630"
/note="Description of /
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Pred. No. 2.6e-156;
0; Mismatches 85;
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Proteomic screen to identify disease-related biological moleculesand inhibitors thereto Patent: WO 2004007717-A 27 22-JAN-2004;
Xerion Pharmaceuticals AG (DE)
Location/Qualifiers
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TTACTGCCATCAGCGGAGTAGTTACCCGCTCACGTTCGGTGCTGGGACACAGTTGGAAAT
                                                              GTCTGGGACCTCTTATTCTCTCACAATCAGCAGCATGGAGGCTGTAGATGCTGCCACTTA 650
                                                                                                                           ATGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGG
                                                                                                                                                                                      CAGCTCAAGTATAAGTTACATGCACTGGTACCAGCAGAAGCCTGTCACCTCCCCCCAAAAG
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                                                                                                        ATGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGG
                                                                                                                                                                   CAGCTCAAGTGTAAGTTACATGCACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAG
                                                                                                                                                                                                                             CCAGTCTCCAGCCATCACAGCTGCATCTCTGGGGCAAAAGGTCACCATCACCTGCAGTGC
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                                             GTCTGGGACCTCTTACTCTCACAATCAGCAGCATGGAGGCTGAAGATGCTGCCACTTA
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Description of Artificial Sequence: scFv"
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Search completed: February 18, 2005, 22:25:56 Job time : 3234.76 Becs

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Result
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Aa151099 Human neu
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Ac83315 Single ch
Adt91208 Single ch
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502.8	502.8	502.8	503	503.6	504	504	504.6	504.6	507.2	508	512	512.6	515	515.8	515.8	517.4	517.4	517.8	520.4	520.6	•	521.8	523.2	523.8
70.1	70.1	70.1	70.2	70.2	70.3	70.3	70.4	70.4	70.7	70.9	71.4	71.5	71.8	71.9	71.9	72.2	72.2	72.2	72.6	72.6	72.7	72.8	73.0	73.1
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ALI GNMENTS

RESULT 1
AAT86309
ID AAT8 20-MAR-1997; Synthetic pro-drug converting Antibody construct; disialoganglioside; GD2; single chain Fv fragment; scFv; tumour; neuroblastoma; osteosarcoma; soft tissue sarcoma; tissue imaging; target delivery; toxin; streptavidin; Single chain anti-disialoganglioside GD2 antibody 5F11-scFv. AAT86309 standard; DNA; 717 25-SEP-1997. WO9734634-A1 06-APR-1998 AAT86309; (first entry) 97WO-US004427 enzyme; GD2-targeted lymphocyte; 88 ВР

Cheung NV, Larson SM, Guo H,

Rivlin K,

Sadelain

(SLOK)_ SLOAN KETTERING INST CANCER RES.

WPI; 1997-479996/44.

20-MAR-1996;

96US-0013703P

Recombinant single chain anti-disialoganglioside GD2 antibody - useful detect tumour cells expressing GD2 and to target therapeutic agents, e toxins, to such cells.

9.6

Disclosure; Page 11; 31pp; English.

The present sequence encodes a recombinant single chain peptide, 5F11-scFv. The peptide is an antibody construct comprising the variable regions of the heavy and light chains of an antibody against dislaloganglioside (GD2) as a single chain Fv fragment (scFv). GD2 occuin many tumours types including neuroblastoma, osteosarcomas and other soft tissue sarcomas, medulloblastomas, high grade astrocytomas, GD2 occurs

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RESULT 2
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           Anti-disialoganglioside GD2 single chain antibody 5F11 scFv
                                         23-MAY-2002
                                                                                             ABA92026
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                                                                                                                                                                                                                   TCTTATTCTCTCACAATCAGCAGCATGGAGGCTGTAGATGCTGCCACTTATTACTGCCAT
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Pred. No. 1.1e-192;
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Single chain antibody; scFv; antibody; disialoganglioside GD2; antitumour; immunostimulant; neuroblastoma; melanoma; sarcoma; small lung carcinoma; brain tumour; cancer; therapy; imaging;
                                                                                                                                        WPI;
                                                                                                                                                  Sadelain M, Cheung
                                                                                                                                                                 (SADE/)
(CHEU/)
(KRAU/)
                                                                                                                                                                                                 30-SEP-1997;
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                                                                                                                                                             (GUOH/)
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                                                                                                                                                            SADELAIN M.
CHEUNG N V.
KRAUSE A.
GUO H.
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New fusion protein, useful for inducing host immune response, comprises variable region of light chain of an antibody linked to variable region of antibody, CD28 receptor signaling domain and transmembrane domain.

Disclosure; Page 3; 9pp; English.

the construction of the present 5F11 scFv gene using a mouse scFv module/recombinant phage antibody system. The scFv can be used in fusion proteins of the invention which comprise an scFv antibody linked to the human T cell surface receptor CD28. T cells expressing such fusion proteins exhibit enhanced survival when reintroduced to an in vivo environment. They can be used to induce an immune response to cells that express the antigen to which the antibody is specific. Cells expressing a fusion protein including an anti-GD2 scFv are useful for treatment of melanomas, neuroblastomas, small lung carcinoma, sarcomas and brain tumours that express GD2 as a surface antigen. Cells expressing the fusion proteins of the invention can also be used for in vitro purging of stem cells or bone marrow and for in vivo targeting of tumour cells and The present sequence is that of cDNA encoding a single chain scFv antibody that is derived from an anti-disialoganglioside GD2 antibody produced by SF11 hybridoma cells. The scFv comprises the SF11 variable chains in VH-VL orientation. mRNA from SF11 hybridoma cells was used in antigen-bearing cells for imaging Ģ,

Sequence 717 BP; 180 A; 181 C; 195 G; 159 T; 0 U; 2 Other;

Similarity

99.7%;

1.1e-192;

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             ATGGAGCTCCGCAGCCTGACATCTGAGGATTCTGCAGTCTATTACTGTGCAAGAGATACT
                                                         AAGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTAC
                                                                                          TCCTGCAAGACTTCTGGANACAAATTCACTGAATACACCATGCACTGGGTGAAGCAGAGC
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ATGGAGCTCCGCAGCCTGACATCTGAGGATTCTGCAGTCTATTACTGTGCAAGAGATACT
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tissue imaging; target delivery; toxin; streptavidin;
pro-drug converting enzyme; GD2-targeted lymphocyte; ss.
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Recombinant single chain anti-disialoganglioside GD2 antibody - useful
                                               WPI; 1997-479996/44
                                                                                                                                                                                 20-MAR-1996;
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                                                                                                                                                                                                                                                                          25-SEP-1997
                                                                                                                                        (SLOK ) SLOAN
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detect tumour cells expressing GD2 toxins, to such cells. and to target therapeutic agents, e.g

Page 12; 31pp; English

The present sequence encodes a recombinant single chain peptide, 5F11scrv-streptavidin. The peptide is an antibody construct comprising the
variable regions of the heavy and light chains of an antibody against
disialoganglioside (GD2) as a single chain Fv fragment (scFv). GD2 occurs
in many tumours types including neuroblastoma, osteosarcomas and other
soft tissue sarcomas, medulloblastomas, high grade astrocytomas,
melanomas and small cell lung cancer. The peptide can be detectably
labelled, preferably with 99m-TC, for tissue imaging of cells expressing
GD2. It can also be used to target delivery of a therapeutic or pretherapeutic agent, such as a toxin, streptavidin (e.g. present sequence)
or a pro-drug converting enzyme, to cells expressing GD2. The peptide may
further comprise CD8 to facilitate the formation of GD2-targeted
characterian therapeutic calls containing the peptide can also be used to target GD2-producing tumour cells

Sequence 1175 BP; 276 A; 346 C; 330 G; 221 T; 0 U; 2 Other;

Length 1175

δ 밁 á 밁 S 밁 ð 밁 Ş 밁 5 밁 Ś 밁 Ś 밁 S 밁 8 밁 S В ફ Matches Query Match Best Local Similarity 716; Conservative 661 601 541 541 481 421 421 361 361 301 301 241 241 181 181 121 121 601 481 61 61 _ 1 CAGGTGAAACTGCAGCAGTCAGGACCTGAACTGGTGNAGCCTGGGGCTTCAGTGAAGATA GACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACC CAGCGGAGTAGTTACCCGCTCACGTTCGGTGCTGGGAACACAGTTGGAAATAAAACGG ATAAGTTACATGCACTGGTACCAGCAGAAGCCTGTCACCTCCCCCAAAAGATGGATTTAT GCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGGCAGCTCAAGT AAGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTAC TCCTGCAAGACTTCTGGANACAAATTCACTGAATACACCATGCACTGGGTGAAGCAGAGC GCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGGCAGCTCAAGT ACGGTCCCGTTTGCTTACTGGGTCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGAGGC ACGGTCCCGTTTGCTTACTGGGTCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGAGGC ATGGAGCTCCGCAGCCTGACATCTGAGGATTCTGCAGTCTATTACTGTGCAAGAGATACT CAGGTGAAACTGCAGCAGTCAGGACCTGAACTGGTGNAGCCTGGGGCTTCAGTGAAGATA **ATAAGTTACATGCACTGGTACCAGCAGAAGCCTGTCACCTCCCCCAAAAAGATGGATTTAT** ATGGAGCTCCGCAGCCTGACATCTGAGGATTCTGCAGTCTATTACTGTGCAAGAGATACT AAGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTAC 98.0%; 99.9%; 0 Score 703; DB 2; Pred. No. 3.5e-189; 0; Mismatches 0; 0 Indels ۲. Gaps 717 659 660 600 600 540 540 480 480 420 420 360 360 300 300 240 240 180 180 120 120 60 60

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                                                                                                                                                                                                                                                   This sequence encodes scFv 508F heavy chain, linker and light chain. The CC scFv fragment was derived from the 508 IgM hybridoma which is generated cC from splenocytes of a mouse that has been immunised with a peptide CC corresponding to the 16 amino terminal residues of beta-Ap conjugated to CC keyhole limpet hemocyanin used a carrier. The resultant variable chain CC fragments may be used in the method of the invention. Cys 96 of the VL CC fragment was replaced with various amino acids to see if production yield CC or stability were effected without having an adverse effect on its CC binding affinity. The invention provides an agent for treating a plaque CC vehicle and are capable of eliciting antibodies capable of disaggregating CC the aggregating protein and/or of preventing aggregation of the CC aggregating protein and/or of preventing aggregation of the CC disease, late onset Alzheimer's diseases, e.g. early onset Alzheimer's CC disease, SAA amyloidosis, hereditary Icelandic syndrome, senility, CC multiple myeloma, scrapie, bovine spongiform encephalopathy (BSE), kuru, CC (GSS) and fatal familial insomnia (FFI)
                                                                                        Query Match
Best Local S
Matches 646
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29-DEC-1999;
31-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating amyloidgenic disease such as Alzheimer's disease, BSE or comprises presentation of plaque derived antigens or epitopes on display vehicle, and introducing the vehicle into the recipient.
                                                                                                                                                                                                         Sequence
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                                                                                                                                             Gene; ds; vaccine; gene therapy; neurological disease; CNS disorder; central nervous system disorder; olfactory system; Alzheimer's disease; Creutzfeld-Jakob disease; Huntington's chorea; Parkinson's disease; viral infection of the brain; brain tumour; lysosomal storage disease;
                                                                                                                                  multiple sclerosis.
                                                                                                                                                                                                          Human neurological/CNS disease treatment method-related
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Best Local
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Alzheimer'd disease; Creutzfeld-Jakob disease; Huntington's chorea; viral infections of the brain; brain tumours; lysosomal storage diseases; Parkinson's disease; and multiple sclerosis. The present DNA sequence represents a gene which was used in the invention
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                                                                                                                       CCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGGCAGCTCA
                                                                                                                                                            ACTACGGTCCCGTTTGCTTACTGGGTCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGA
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                          TATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGG
                                                                                                       CCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCA
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RESULT 6
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29-DEC-1999;
31-JUL-2000;
31-AUG-2000;
15-MAR-2001;
07-AUG-2001;
12-APR-2002;
06-JUN-2002;
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)B; ADJ88113.
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; 2000US-01800518.
; 2001US-00808037.
; 2001US-00830954.
; 2002US-0371735P.
; 2002US-00162889.
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99US-00473653.
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/product= "508 antibody heavy chain
/partial
/note= "No start and stop codon"
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Treating ne displaying display veh ing therapeutic vehicle which i neurological disease CNS e.g., Alzheimer's disease, by ng therapeutic molecule capable of treating the disease on viral vehicle which is then administered to subject through olfactory

Example 2; SEQ Ħ ĕ <u>ن</u> 68pp; English.

The invention relates to a method of treating a neurological disease of disorder of the central nervous system (CNS). The method involves displaying a therapeutic molecule capable of treating the neurological disease or disorder of the CNS on a viral display vehicle and introductiviral display vehicle into a subject by applying an effective amount of the viral display vehicle displaying the therapeutic molecule to an introducing amount of õ

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RESULT 7
ACC83315
ID ACC8
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90.1%;
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Pred. No. 4e-158;
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                                                                                                                                                                          tumour is a primary or a metastasized tumour such as carcinoma of the bladder, breast, cervix, colorectum, lung, ovary, pancreas, prostate, stomach, cholangiccarcinoma, gastric sarcoma, glioma, lymphoma, melanoma, multiple myeloma, osteosarcoma, head and neck tumor and solid tumor. The method of the invention is useful for X-ray-guided delivery of a therefore the invention, a diagnostic composition or their combinations to a tumour in a subject. The current sequence represents a single chain antibody encoding sequence that was identified following in vivo panning to irradiated tumours. This antibody binds platelet membrane glycoprotein
                                                                                                                                                                                                                                                                                                                      The invention relates to a method for identifying a molecule that binds an irradiated tumour in a subject. The method of the invention involves exposing a tumour to ionizing radiation, administering a library of diverse molecules to a subject, and isolating one or more molecules of the library from the tumour. The method of the invention is useful for identifying a molecule that binds an irradiated tumour in a subject e.g. warm-blooded vertebrate and human, and also for tumour detection. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying molecule that binds to irradiated tumor in a subject, exposing tumor to ionizing radiation, administering library of dimolecules and isolating library molecules from tumor to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cervix; colorectum; lung; ovary; pancreas; prostate; stomach; cholangiocarcinoma; gastric sarcoma; glioma; lymphoma; melanoma; multiple myeloma; osteosarcoma; head; neck; radiation; x-ray; gene;
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cervix; colorectum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour; benign intracranial meningioma; arteriovenous
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CC The invention relates to a method for screening phage-displayed CC antibodies binding to radiation-inducible neoantigen on cell. The method CC involves contacting cell with antibodies, treating cell with radiation, CC contacting cell with antibodies not binding to cell and detecting the CC contacting cell with antibodies not binding to cell and detecting the CC displayed antibodies for an ability to bind to a radiation-inducible CC neoantigen present on a cell, where the cell is tumour cell chosen from CC benign intracranial meningiomas, arteriovenous malformation, angioma, CC macular degeneration, melanoma, adenocarcinoma, malignant glioma, CC carcinoma, thyroid carcinoma, bladder carcinoma, pancreatic CC carcinoma, brain carcinoma, liver carcinoma, colon carcinoma, rectal CC carcinoma, solid tumours, solid tumour metastases, angiofibromas, CC carcinomas, solid tumours, solid tumour metastases, angiofibromas, cC carcinomas and their combinations or vascular endothelial cell. The present sequence is a DNA encoding single chain variable fragment (scFv) antibody that binds to radiation-inducible neoantigens.
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09-NOV-2001;
27-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; SEQ ID NO 19; 64pp; English.
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; 2001US-00914605.
; 2002US-00259087.
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            ATGGAGCTCCGCAGCCTGACATCTGAGGATTCTGCAGTCTATTACTGTGCAAGA---GAT
                                                                                                                                           AAGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTAC
                                                                                                                                                                      CCTGGGCAGGGCCTTGAGTGGATTGGATATATTAATCCTTACAATGATGGTACTAAGTAC
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                                          AACTACGGTGCTTTGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGA
                                                      ACTACGGTCCCGTTTGCTTACTGGGTCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGA
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1.3e-152;
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RESULT 9
AAF61510
ID AAF6
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                Cell-targeting vector selective for T lymphocytes, useful in gene to of e.g. acquired immune deficiency syndrome, encodes a single-chain variable antibody fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tlymphocyte; antibody; single chain variable antibody; scFv; human; cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS; gene therapy; immunization; diagnosis; T cell-associated disease; SCID; acquired immune deficiency syndrome; severe combined immune deficiency;
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Spleen necrosis
Chimeric.
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25-JUN-2001
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/note= "No stop codon given"
136. .927
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/note= "no stop codon given"
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Claim 1; Fig 2; 18pp; German.

This invention describes a novel cell-targeting vector (A) containing a CC DNA sequence (I) encoding a single-chain variable antibody fragment (C (scFv). The products of the invention have antivital, cytostatic and cimmunostimulant activity and can be used in gene therapy, immunization CC and diagnosis particularly of T cell-associated diseases, specifically C acquired immune deficiency syndrome (AlDS), severe combined immune CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently of the CD4 receptor, with high selectivity, 4-5 fold selectivity over CC designated 7A5 encodes a 329 amino acid single-chain variable antibody CC fragment, fully defined in the specification. It was used to transform CC (SNV)) cells, CB166 (human T lymphocyte) cells, and HeLa (human cervical carcinoma) cells. After 48 hours, the cells were stained with X-gal to CC determine transformation. The viral titer (infectious units/ml) was over CC inillion for D17, inillion for CB166 but less than 100 for HeLa, CC SNV-env leader/human K6-scFv fusion construct used in the construction of CC convel cell targeting vectors described in the invention. (Updated on 11-cx CC SEP-2003 to standardise OS field)

Sequence 927 BP; 205 A; 238 C; 277 G; 207 T; 0 U; 0 Other;

Similarity

79.3%;

Score 568.4; Pred. No. 5.6

; DB 5;

Length 927;

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RESULT 10
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The invention relates to a method for screening phage-displayed antibodies binding to radiation-inducible necentiagen on cell. The method involves contacting cell with antibodies, treating cell with radiation, contacting cell with antibodies not binding to cell and detecting the bound antibody. The method is useful for screening several phage-in the contacting cell with antibodies not binding to cell and detecting the contacting antibody. The method is useful for screening several phage-in the contacting present on a cell, where the cell is tumour cell chosen from the contacting intracranial meningioma, arteriovenous malformation, angioma, compared the contacting antibody. The method is useful for screening several phage-in contacting intracranial meningioma, arteriovenous malformation, angioma, compared to grostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic corrections, thyroid carcinoma, lung carcinoma, bladder carcinoma, pancreatic corrections, brain carcinoma, liver carcinoma, breast carcinoma, ovary carcinoma, solid tumours, solid tumour metastases, angiotibromas, corrected corrected fibroplasias, haemangiomas, Kaposi's sarcoma, head and neck carcinomas and their combinations or vascular endothelial cell. The correct carcinoma is a DNA encoding single chain variable fragment (scFv) cantibody that binds to radiation-inducible neoantigens.
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09-NOV-2001;
27-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                                                                     Screening phage-displayed antibodies binding to radiation-inducible neoantigen on cell, comprises contacting cell with antibodies, treating cell with radiation, contacting cell with antibodies not binding to cell, detecting bound antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liver carcinoma; breast carcinoma; ovary carcinoma; angiofibroma; retrolental fibroplasia; haemangioma; Kaposi's sarcoma; single chain variable fragment; scFv; gene; ds.
                                                                                                                                                                                                                                                                                                                                                   Claim
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)B; ADT91213.
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2001US-00914605.
2002US-00259087.
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antibody"
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RESULT 11
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AC ADC79
XX DT 01-JJ
DT VX-8-
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Best Local'Similarity
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                     antigen; CA 125 tumour antigen modulator;
          antigen-associated
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Query Match
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(1) a recombinant nucleic acid comprising at least one sequence selected from the group consisting of ADC79233, ADC79235, ADC79235, ADC79236, ADC79238; (2) a vector comprising the recombinant nucleic acid; (3) a host cell; (4) a pharmaceutical composition; (5) preventing or treating CA 125 tumour antigen-associated disease in a mammal; and (6) negatively modulating a CA 125 tumour antigen in a mammalian cell. A modulator capable of negatively modulating a CA 125 tumour antigen in a mammalian cell. A cytostatic activity, and can be used in gene therapy. The modulator, recombinant nucleic acid, vector or host cell can be used for preparing a composition for preventing or treating CA 125 tumour antigen-associated disease in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7;
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28-FEB-2003; 2003CA-02420494.
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reating CA
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CCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGGCAGCTCA
                                                                                   GGGTTTTGGTACTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGA
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The invention relates to a method for identifying a molecule that binds an irradiated tumour in a subject. The method of the invention involves exposing a tumour to ionizing radiation, administering a library of diverse molecules to a subject, and isolating one or more molecules of the library from the tumour. The method of the invention is useful for identifying a molecule that binds an irradiated tumour in a subject e.g. warm-blooded vertebrate and human, and also for tumour detection. The

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                                                                                                                                                                                                                                                                         Identifying molecule that binds to irradiated tumor in a subject, by exposing tumor to ionizing radiation, administering library of diverse molecules and isolating library molecules from tumor to identify the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cervix; colorectum; lung; ovary; pancreas; prostate; stomach;
cholangiocarcinoma; gastric sarcoma; glioma; lymphoma; melanoma;
multiple myeloma; osteosarcoma; head; neck; radiation; x-ray; gene;
                                                                                                                                                                                                        Claim
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Matches 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumour is a primary or a metastasized tumour such as carcinoma of the bladder, breast, cervix, colorectum, lung, ovary, pancreas, prostate, stomach, cholangiocarcinoma, gastric sarcoma, glioma, lymphoma, melanoma, multiple myeloma, osteosarcoma, head and neck tumor and solid tumor. The method of the invention is useful for X-ray-guided delivery of a theorem tion, a diagnostic composition or their combinations to a tumour in a subject. The current sequence represents a single chain antibody encoding sequence that was identified following in vivo panning to irradiated tumours. This antibody binds P-selectin
                16-DEC-2004
                                                                       ADT91206
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28-APR-2000;
09-NOV-2001;
27-SEP-2002;
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                                                                                                                                                                                                                      Claim 4; SEQ ID NO 17; 64pp; English.
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2002US-00259087
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/note= "No
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The invention relates to a method for screening phage-displayed CC antibodies binding to radiation-inducible neoantigen on cell. The method CC involves contacting cell with antibodies, treating cell with radiation, CC contacting cell with antibodies not binding to cell and detecting the CC bound antibody. The method is useful for screening several phage-cC displayed antibody. The method is useful for screening several phage-cC neoantigen present on a cell, where the cell is tumour cell chosen from CC benign intracranial meningiomas, arteriovenous malformation, angioma, CC macular degeneration, melanoma, adenocarcinoma, malignant glioma, CC prostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic carcinoma, thyroid carcinoma, liver carcinoma, breast carcinoma, ovary CC carcinoma, boild tumours, solid tumour metastases, angiofibromas, cretal cretrolental fibroplasias, haemangiomas, Kaposi's sarcoma, head and neck CC carcinomas and their combinations or vascular endothelial cell. The CC carcinomas and their combinations or vascular endothelial cell. The CC carcinoma is a DNA encoding single chain variable fragment (scFv) cantibody that binds to radiation-inducible neoantigens.

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Query Match
Best Local :
         Similarity
         86.4%;
                  77.2%;
Pred. No. 1.1
D; Mismatches
                  Score
        1.1e-146;
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Matches

Sequence

726

BP; 173

A; 188 C;

202 G; 163 T; 0 U;

0 Other;

밁 S 622; CAGGTGAAACTGCAGCAGTCTGGGGGCTTGAGCTTGATGCCTGGGGGCTTCAGTGAAGATG CAGGTGAAACTGCAGCAGTCAGGACCTGAACTGGTGNAGCCTGGGGGCTTCAGTGAAGATA 0, Indels ω •• 60 66 ۲

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                                                         AGCGGAGTAGTTACCCGCTCACGTTCGGTGCTGGGACACAGTTGGAAATAAAACGG
                                                                                                                              CTTATTCTCTCACAATCAGCAGCATGGAGGCTGTAGATGCTGCCACTTATTACTGCCATC
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                                                                                                                                                                                                   ACACATCCAAACTGGCTTCTGGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGGACCT
                                                                                                                                                                                                                                                                          TAAGTTACATGCACTGGTACCAGCAGAAGACCTGTCACCTCCCCCAAAAGATGGATTTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGTCCCGTTTGCTTACTGGGTCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGAGGCG
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85.2%;
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Pred. No. 4.3e-145;
0; Mismatches 106;
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The present sequence is a DNA encoding anti-hepatitis B surface antigen (4C2) scFv. It can be fused upstream of the DNA encoding light chain constant region of mouse antibody 1C3 or other gene of interest in a DNA construct, for ribosome display. The DNA construct is generated for producing replicable mRNA molecules that are used in continuous cyclic process of replication, mutation, and translation leading to continuous in vitro evolution (CIVE) of mutant proteins. This method is useful for generating proteins with improved diagnostic and therapeutic properties mutation, synthesis

2 AGGTGAAACTGCAGCAGTCAGGACCTGAACTGGTGNAGCCTGGGGCTTTCAGTGAAGATAT TGGAGCTCCGCAGCCTGACATCTGAGGATTCTGCAGTCTATTACTGTGCAAGAGATACTA ACCAGAAGTTTGAGGCCAAGGCCACAATGACTGTAGACAAATCCTCCAACACAGGCTATT AGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTACA ATGCCAAGAGTCTAGAGTGGATTGGACTTATTAGTAATTCCTTTGGTAATACAAACTACA CCTGCAAGGGTTCCGGCTACACATTCACTGATTATGCTATGCATTGGGTGAAGCAGAGTC | CCTGCAAGACTTCTGGANACAAATTCACTGAATACACCATGCACTGGGTGAAGCAGAGCC ATGTGAAGCTTCAGGAGTCAGGGCCTGAGCTGGTGAGGCCCGGGGTCTCAGTGAAGATTA Indels Length 0; Gaps 69 301 249 241 181 129 121 61 189

717

98 661 509 601 549 541 489 481 369 361 309

DNA

stemloop;

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CC with a translation system, forming a population of mutant protein/mRNA CC complexes and selecting one or more complex(es) by exposing the CC population of mutant protein/mRNA complexes to the target molecule and CC population of mutant protein/mRNA complexes to the target molecule and CC element which promotes transcription of the DNA into mRNA and a ribosome binding site, a cloning site location downstream of the untranslated CC region, and a replicase binding sequence located upstream of the cloning control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to mutating, synthesising and selecting a protein which binds to a target molecule, comprising incubating replicable a mRNA molecule encoding the protein with ribonucleoside triphosphate precursors of RNA and an RNA-directed RNA polymerase, where the polymerase replicates mRNA molecule and introduces mutations, incubating the mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing mut
protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIVE; RNA-directed RNA polymerase; ribosome binding site;
untranslated region; replicase binding sequence; MDV-1; RQ135;
Obeta replicase; Hepatitis C RNA-directed RNA polymerase; NS5B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; antibody; glycophorin; CIVE; RNA-directed RNA polymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutant protein, by incubating replicable mRNA molecule en
ith ribonucleoside triphosphate precursors of RNA and RNA-
RNA polymerase, incubating mutants with translation system
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Matches 610
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                                                                   CTTATTCTCTCACAATCAGCAGCATGGAGGCTGTAGATGCTGCCACTTATTACTGCCATC
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85.2%;
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Search completed: February Job time: 424.878 secs 18,

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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
          593.4
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APPLICANT: Cheung, Nai-Kong V.
APPLICANT: Guo, Hong-Fen
APPLICANT: Guo, Hong-Fen
APPLICANT: Rivlin, Ken
APPLICANT: Rivlin, Ken
APPLICANT: Sadelain, Michel
TITLE OF INVENTION: Single Chain FV Constructive of INVENTION: Michel
TITLE OF INVENTION: Antibodies
FILE REFERENCE: MSK.P-013-USNP
CURRENT APPLICATION NUMBER: US/09/142,974B
CURRENT APPLICATION NUMBER: US/09/142,974B
CURRENT FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: PCT/US97/04427
PRIOR APPLICATION NUMBER: 60/013,703
PRIOR FILING DATE: 1996-03-20
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Patent No. 6451995
GENERAL INFORMATION:
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SEQ ID NO 3
                 Query Match 99.7%; Score 715; DB 3; Length 1176; Best Local Similarity 100.0%; Pred. No. 4.3e-198; Matches 717; Conservative 0; Mismatches 0; Indels
                                                                                        OTHER INFORMATION: 5
NAME/KEY: unsure
LOCATION: (37)
NAME/KEY: unsure
LOCATION: (79)
                                                                                                                                                                      LENGTH: 1176
TYPE: DNA
ORGANISM: Murine
FEATURE:
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; SOFTWARE: PatentIn vers
; SEQ ID NO 5
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Artificial seq
; PEATURE:
; PEATURE:
; NAME/KEY: misc feature
; LOCATION: ()...()
; OTHER IMPORMATION: 8CFV
US-09-473-653-5
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                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09473653 Patent No. 6703015 GENERAL INFORMATION:
                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/473,653
CURRENT FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/152,417
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                 APPLICANT: Solomon, Bek
APPLICANT: Frenkel, Dan
TITLE OF INVENTION: IMV
FILE REFERENCE: 00/2078
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Query Match Best Local Similarity Matches 646; Conserv

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Sequence 1, Application US/09581345
; Patent No. 6809184
; Patent No. 6809184
; Patent INFORMATION:
; APPLICANT: Pasten, Ira H.
; APPLICANT: Chowdhury, Partha S.
; APPLICANT: The Government of the United States
; APPLICANT: as represented by The Secretary of the
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Antibodies, Including Fv Molecules, and
; TITLE OF INVENTION: Mesothelin and Methods for Their Use
; TITLE OF INVENTION NUMBER: US/09/581,345
; CURRENT APPLICATION NUMBER: US/09-27
; PRIOR APPLICATION NUMBER: US 60/067,175
; PRIOR APPLICATION NUMBER: WO PCT/US98/25270
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90.1%; Pred. No. 9e-163;
tive 0; Mismatches 6
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 RESULT 5
US-09-674-677-4
US-09-674-677-4
; Sequence 4, Application US/09674677
; Patent No. 6562622
; GENERAL INFORMATION:
; APPLICANT: Coia, et al.
; TITLE OF INVENTION: CONTINUOUS IN-VITRO EVOLUTION
; PILE REFERENCE: 674537-2003
; CURRENT APPLICATION NUMBER: US/09/674,677
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; OTHER INFORMATION:
US-09-581-345-1
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NUMBER OF SEQ ID NOS: 9
SOPTWARE: PatentIn Ver.
SEQ ID NO 1
LENGTH: 723
TYPE: DNA
ORGANISM: Artificial S
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nilarity 89.7%;
Conservative
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RESULT 4 US-09-581-345-1

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LENGTH: 807
; TYPE: DNA
; ORGANISM: Homo Sapeins
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(807)
; OTHER INFORMATION: Sequence of
; Patent No. 6562622
US-09-674-677-4
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PRIOR APPLICATION NUMBER: PCT/AU99/00341
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: AU PP3445
PRIOR FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 38
SOPTMARE: PATENTIN VETSION 3.0
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                                                                  AGCGGAGTAGTTACCCGCTCACGTTCGGTGCTGGGACACAGTTGGAAATAAAACGG
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RESULT 7 US-09-526-738A-3

Sequence 3, Application US/09526738A

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; LENGTH: 771
; TYPE: DNA
; ORGANISM: Humanus
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Patent No. 6630584

GENERAL INFORMATION:
APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DVELOPMENT APPLICANT: LTD.
APPLICANT: LTD.
TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
FILE REFERENCE: 1196336
CURRENT APPLICATION NUMBER: US/09/526,738A
CURRENT FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
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Best Local Similarity
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CAGCGGAGTAGTTACCCGCTCACGTTCGGTGCTGGGACACAGTTGGAAATAAAACGG 717
                                                        TCTTACTCTCTCACAATCAGCCGGATGGAGGCTGAAGATGCTGCCACTTATTACTGCCAG
                                                                               TCTTATTCTCTCACAATCAGCAGCATGGAGGCTGTAGATGCTGCCACTTATTACTGCCAT
                                                                                                               AGCACATCCAACCTGGCTTCTGGAGTCCCTGCTCAGTGGCAGTGGATCTGGGACC
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Pred. No. 1.6e-145;
0; Mismatches 105;
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; Patent No. 6630584;
GENERAL INFORMATION;
APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLICANT: LTD.
TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGFILE REFERENCE: 1196336;
CURRENT APPLICATION NUMBER: US/09/526,738A;
CURRENT FILLING DATE: 2000-03-16;
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 780
TYPE: DNA
ORGANISM: Humanus
RESULT 8
US-09-798-689-22
; Sequence 22, Application US/09798689
; Patent No. 6811779
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                                                                                                      CAAAGGAGTAGTTACCCATACACGTTCGGAGGGGGCACCAAGCTGCAAATCAAACGG
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84.9%;
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Pred. No. 1.6e-145;
0; Mismatches 105;
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CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/401,163
PRIOR FILING DATE: 1999-09-22
PRIOR PELICATION NUMBER: 08/967,113
PRIOR FILING DATE: 1997-11-08/706,804
PRIOR APPLICATION NUMBER: 08/706,804
PRIOR FILING DATE: 1996-09-03
PRIOR PILING DATE: 1996-09-03
PRIOR PILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/476,533
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/326,552
PRIOR FILING DATE: 1994-02-10
PRIOR PILING DATE: 1994-02-10
PRIOR FILING DATE: 1994-02-10
PRIOR FILING DATE: 1994-02-10
PRIOR FILING DATE: 1994-02-10
NUMBER OF SEQ ID NOS: 41
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; ORGANISM: Mouse
US-09-798-689-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SOFTWARE: Par
; SEQ ID NO 22
; LENGTH: 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 73.4%; Score 526.4; DB 4; Best Local Similarity 83.5%; Pred. No. 2.9e-143; Matches 596; Conservative 0; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Rockwell, Patricia
APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF ATTLE OF INVENTION: Combined With Radiation and Chemotherapy
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
Patent No. 6811779
                                                                                                                                                 421
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                                      GACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTTGGGACC
                                                                                                      ATAAGTTACATGCACTGGTACCAGCAGAAGCCTGTCACCTCCCCCAAAAGATGGATTTAT
                                                                                                                                                                                                                                                                             GGTGACTACGAAGGCTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGAGGC
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                                                                                                                                                                                                                                   CCTGAACAGGGCCTGGAGTGGATTGGATTGATCCTGAGAATGGTGATTCTGATTAT
                                                                                                                                                   GCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATAACCTGCAGTGCCAGCTCAAGT
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Indels Length

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US-09-486-814A-1
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LENGTH: 894
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APPLICANT: YAMAMOTO, MASATO
APPLICANT: HAYAGHI, NO. 656259910
APPLICANT: YAMAMOTO, Hiroko
APPLICANT: YOHDOH, Naoki
TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS
TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC
TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
FILE REFERENCE: 0020-4682P
CURRENT APPLICATION NUMBER: US/09/486,814A
CURRENT FILING DATE: 2002-06-13
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                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                              Matches 624;
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SOFTWARE: PatentIn Ver. ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Mus sp., strain: Balb/c, tissue:
PEATURE:
OTHER INFORMATION: Clone: pZeoSVIC9
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1)..(894)
OTHER INFORMATION: strandedness:
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OTHER INFORMATION: Encoding
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LOCATION: (1). (111)
OTHER INFORMATION: Encoding
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LOCATION: (1)...(891)
OTHER INFORMATION: Identification Method:
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                                                                                                                                                                                                                                                                                          y Match 73.1%;
Local Similarity 85.6%;
nes 624; Conservative
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                                                                    ATGGAAAGAGCCTTGAGTGGATTGGATATTTATCCTTACAATGGTGGTACTGGCTAC
                                                                                                                                                                                                                    CAGGTGAAGCTGCAGGAGTCAGGACCTGAGCTGGAGAAGACCCTGGCGCTTCAGTGAAGATA
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                      AAGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTAC
                                                                                                TCCTGCAAGACTTCTGGANACAAATTCACTGAATACACCATGCACTGGGTGAAGCAGAGC
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 AACCAGAAGTTCAAGAGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTAC
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Pred. No. 1.8e-142;
0; Mismatches 84;
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US-08-553-497A-25
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                                               STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: KETTLE
APPLICANT: BENDIG
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
CLASSIFICATION: 530 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                      ADDRESSEE:
STREET: 22:
CITY: ARLII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08553497A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KETTLEBOROUGH, C. I
BENDIG, MARY M.
ANSELL, KEITH H.
GUSSOW, DETLEF
                                                                                                                                                                                                                                                                         3: MILLEN, WHITE, ZELANO & BRANIGAN, 2200 CLARENDON BLVD. SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                  ROSELL, ELISABET
BLASCO, FRANCESC
PIULATS, JAUME
                                                                                                                                                                                                                                                                                                                                                                                                                                         MITJANS, FRANSESC
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 WO PCT/EP95/00978
                                                                                                            Version
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TELEPAX: 703-245-0...
INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 941189
EILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33302
REFERENCE/DOCKET NUMBER: MERC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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   CLONE: 5 F 1 (single-chain Fv, heavy, light chain,
   CLONE: linker)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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STRAIN: Balb/c
TISSUE TYPE: splenocytes
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GGCAGCTCAAGTATAAGTTACATGCACTGGTACCAGCAGAAGCCTGTCACCTCCCCCAAA 528
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                                                                                                                       TCAGGTGGAGGCGGTTCAGGCGGAGGTGGCTGGCGGTGGCGGATCGGACATCGAGCTC 408
                                                                                                                                                                TATGATTACGACGGACGGTACTTTGACTACTGGGGCCAAGGGACAACGGTCACCGTCTCC
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                               ACCCAGTCTCCAACAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGT
                                                  ACTCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGT 468
                                                                                                  TCAGGTGGCGGTGGCTCGGGTGGTGGGTGGCGGCGGATCTGACATTGAGCTC
                                                                                                                                                                                               TACGGTCCCG-----TTTGCTTACTGGGTCCAAGGGACCACGGTCACCGTCTCC 348
                                                                                                                                                                                                                                  ATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCCAGTCGGGAC
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84.4%;
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Pred. No. 7.2e-142;
0; Mismatches 101;
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RESULT 11
US-08-463-163-2
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Patent No. (
                                                                                                            SOFTWARE: Patentin Release #1.0, Vet CURRENT APPLICATION NUMBER: US/08/463,163 FILING DATE: 05-JUN-1995 CLASSIFICATION DATA: 05-JUN-1995 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 06/22,227 FILING DATE: 2-JAN-1981 PRIOR APPLICATION NUMBER: US 06/911,227 FILING DATE: 24-SEP-1986 PRIOR APPLICATION NUMBER: US 07/341,361 FILING DATE: 21-APR-1989 PRIOR APPLICATION NUMBER: US 07/341,361 FILING DATE: 21-APR-1989 PRIOR APPLICATION NUMBER: US 07/865,722 FILING DATE: 08-APR-1992 ATTORNEY/AGENT INFORMATION: NAME: Weber, Ellen L. REGISTRATION NUMBER: 032762 REFERENCE/DOCKET NUMBER: 035280-1221 TELECOMMUNICATION INFORMATION: TELEEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1797 base pair
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ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Waldmann, Thom
APPLICANT: Queen, Cary L.
TITLE OF INVENTION: Recom
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TYPE: nucleic acid
STRANDEDNESS: sing
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                                    1797 base pairs
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                                                                                                      (415)
                                                                                                    543-5043
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Sequence 7, Application US/08279772A
Patent NO. 6080560
GENERAL INFORMATION:
APPLICANT: Russell, David R
APPLICANT: Fuller, James T
TITLE OF INVENTION: Method for Pr
TITLE OF INVENTION: Cells
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
STREET: PO Box 2113
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US-08-279-772A-7
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Best Local :
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LOCATION: 1..1797
OTHER INFORMATION:
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597; Conserv
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83.7%;
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Pred. No. 1.7e-140;
0; Mismatches 113;
                                                                              Producing
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US-08-279-772A-7
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Best Local &
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FILING DATE
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-229-9097-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEPAX: 608-251-9166
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STATE: WI
COUNTRY: United States of
ZIP: 53701-213
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
COMPUTER: IBM PC compat
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 base pairs
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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Similarity 83.6%;
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   GACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACC
                                                              ATAAGTTACATGCACTGGTACCAGCAGAAGCCTGTCACCTCCCCCAAAAGATGGATTTAT
                                                                                                                GCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGGCAGCTCAAGT
                                                                                                                                                          GGCTCGGGCGGTGGCGGTGGCGGCGCTCTCAAATTGTTCTCACCCAGTCTCCA
                                                                                                                                                                              GGGGTC---TTTGACTACTGGGGCCAAGGAACCACTCTCACAGTCTCCTCCGGAGGCGGT
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Pred. No. 3.5e-140;
0; Mismatches 114;
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US-08-902-486-10
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                                                                                                                                                            Query Match
Best Local Similarity
Matches 596; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEPAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Sday, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 67
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CORRESPONDENCE ADDRESS:
ADDRESSES: Quarles & Brady
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APPLICANT: Fuller, James T.
TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND
TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS
                                                                                                                                                                                                                                                                           FEATURE:
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LOCATION:
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Pred. No. 3.5e-140;
D; Mismatches 114;
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US-08-553-497A-27
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GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                     APPLICANT: BLASCO, FI
APPLICANT: PIULATS,
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                          STREET: 2200 CLA
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
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5844093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGAGCTCCGCAGCCTGACATCTGAGGATTCTGCAGTCTATTACTGTGCAAGAGATACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCACATCCAACCTGGCTTCTGGAGTCCCTGCTCCGCTTCAGTGGCAGTGGATCTGGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGCAACTGAGCAGCCTGACATTTGAGGACTCTGCAGTCTATTACTGTGCAAGAGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATCAGAAGTTCAAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTAC
                                                                                                                                                                                                                                                                                                    MITJANS, FRANSESC
ROSELL, ELISABET
BLASCO, FRANCESC
PIULATS, JAUME
                                                                                                                                                                                                          E: MILLEN, WHITE, ZEI 2200 CLARENDON BLVD.
                                                                                                                                                                                                                                                                                                                                                                                    KETTLEBOROUGH, C. BENDIG, MARY M. ANSELL, KEITH H. GUSSOW, DETLEF
                                                                                                                                                                                                                                                                                                                                                                      ADAN,
                                                                                                                                                                                                                                                                                                                                                                   JAUME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TTTGACTACTGGGGCCAAGGAACCACTCTCACAGTCTCCTCCGGAGGCGGT
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                                                                                                                                                                                                          ZELANO & BRANIGAN,
/D. SUITE 1400
                                                                 Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 703-243-6410
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: mouse
STRAIN: Balb/c
TISSUE TYPE: splenocytes
IMMEDIATE SOURCE:
LIBRARY: 7 G 1 (single-chain Fv, heavy, light chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1..726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: 7 G 1 (
LIBRARY: linker)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: WO PCT/EP95/00978 FILING DATE: 16-MAR-1995
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                                                                                                                                                                                                                                                                                                                                 CCTGCAAGACTTCTGGANACAAATTCACTGAATACACCATGCACTGGGTGAAGCAGAGCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGTGAAACTGCAGCAGTCAGGACCTGAACTGGTGNAGCCTGGGGCTTCAGTGAAGATAT
CCCAGTCTCCAACAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTG
                                                                CAGGTGGCGGTGGCTGGTGGTGGGTGGCGGCGGATCTGACATTGAGCTCA
                                                                                    CAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCA 409
                                                                                                                                ATGATTACGACGGACGGTACTTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCT
                                                                                                                                                                                                 TCGAACTCAGCAGCCTGACATCTGAGGACTGCTCGGTCTATTACTGTGCCAGTCGGGACT
                                                                                                                                                                                                                                TGGAGCTCCGCAGCCTGACATCTGAGGATTCTGCAGTCTATTACTGTGCAAG-AGATACT
                                                                                                                                                                                                                                                                   ATGAGAAATTCAAGAGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACA
                                                                                                                                                                                                                                                                                                                                                                                                   CCTGCAAGGCTTCCGGCTACACCTTCACCAGCCACTTGGATCACTGGGTGAAGCAGAGGG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGTCAAGCTGCAGCAGTCAGGGGCTGAACTGGTGAAGCCTGGGGGCTTCAGTGAAGTTGT
                    CTCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAAAGGTCACCATGACCTGCAGTG
                                                                                                                                                                ACGGTCCCG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 512.6; DB 2;
Pred. No. 3e-139;
                                                                                                                                                               TTTGCTTACTGGGTCCAAGGGACCACGGTCACCGTCTCCT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                              421
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RESULT 15
US-08-652-507-1
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                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/652,507
FILING DATE: 02-Jul-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-211
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                        TELEPHONE: 703-816-400
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Commontary
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 810 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                       TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                       STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Arlington
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542 TTCTGATTTATGACACATCCAACCTGGCTTCTGGAGTCCCTGTTCGCTTCAGTGGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           530 GATGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTG
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                                                    79
                                                                      1 CAGGTGAAACTGCAGCAGTCAGGACCTGAACTGGTGNAGCCTGGGGGCTTCAGTGAAGATA 60
                                                                                                                                                                                                                                                  : 810 base pairs
                                                    CAGGTGAAACTGCAGCAGTCTGGGGCAGAACTTGTGAGGTCAGGGACCTCAGTCAAGTTG
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1100 No. 5876691th Glebe Road, 8th Floor
                                                                                                                       Conservative
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                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                 70.7%;
82.2%;
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                                                                                                                                                                                                                                                                                                           1:
                                                                                                                   Score 507.2; DB 2;
Pred. No. 1.2e-137;
0; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.30 (EPO)
                                                                                                                       Indels
                                                                                                                                                     Length
                                                                                                                                                        810;
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                                                                                                                       Gaps
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Search completed: February 18, 2005, 23:56:46 Job time : 150.31 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
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Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

20: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

21: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

22: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

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24: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

25: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

26: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

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US-08-940-544-3 US-10-075-947A-1 US-10-075-947A-3 US-09-808-037-5 US-10-162-889-5 US-10-384-788-5 US-10-618-856-5 US-10-618-856-5 US-10-689-006-19 US-10-689-006-23 US-10-259-087A-17	SUMMARIES
Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 19, Appli Sequence 19, Appli Sequence 23, Appli Sequence 23, Appli	Description

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ALIGNMENTS

Query Match Best Local Similarity	ESULT 1 S-08-940-544-3 Sequence 3, Application US/08940544B Publication No. US20020018733A1 GENERAL INFORMATION: APPLICANT: SADELAIN, MICHEL APPLICANT: CHEUNG, NAI-KONG V. APPLICANT: KRAUSE, ANJA APPLICANT: KRAUSE, ANJA APPLICANT: KRAUSE, ANJA APPLICANT: WIVENTION: FUSION PROTEINS OF A SINGLE CHAIN ANTIBODY AND CD28 AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: MSK.P-035-US CURRENT PAPLICATION NUMBER: US/08/940,544B CURRENT FILING DATE: 1997-09-30 EARLIER APPLICATION NUMBER: PCT/US97/04427 EARLIER APPLICATION NUMBER: PCT/US97/04427 EARLIER APPLICATION NUMBER: PCT/US97/04427 EARLIER FILING DATE: 1997-03-20 NUMBER OF SEQ ID NOS: 4 SOFTWARE: PATENTIN Ver. 2.0 SEQ ID NO 3 LENGTH: 717 TYPE: DNA ORGANISM: HUMAN FEATURE: OTHER INFORMATION: SF11-scFV FEATURE: NAME/KEY: UNSURE LOCATION: (37) FEATURE: NAME/KEY: UNSURE LOCATION: (79) S-08-940-544-3
99.7%;	US/089 118783AI ICCHEL -KONG V -KONG V -R SIS-US 997-09- 997-09- 997-09- 997-03-: 11-scFV
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DB 8; Length 717; .9e-228;	CHAIN
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Sequence 1, Application US/10075947A
Publication No. US20030147808A1
GENERAL INFORMATION:
APPLICANT: Cheung, Nai-Kong V.
APPLICANT: Larson, Steven M.
APPLICANT: Larson, Steven M.
APPLICANT: Rivlin, Ken
APPLICANT: Rivlin, Ken
APPLICANT: Sadelain, Michel
TITLE OF INVENTION: Antibodies
FILE REFERENCE: MSK: P-013-2
CURRENT APPLICATION NUMBER: US/10/075,947A
CURRENT APPLICATION NUMBER: 09/142,974
PRIOR APPLICATION NUMBER: 09/142,974
PRIOR APPLICATION NUMBER: PCT/US97/04427
PRIOR APPLICATION NUMBER: PCT/US97/04427
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PRIOR FILING DATE: 1997-03-20
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  Sequence 3, Application US/10075947A Publication No. US20030147808A1 GENERAL INFORMATION:
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SEQ ID NO 1
LENGTH: 717
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NAME/KEY: unsure
LOCATION: (37)
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NAME/KEY: unsure
LOCATION: (79)
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ORGANISM: Murine
FEATURE:
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                                        TCTTAITCTCTCACAAICAGCAGCATGGAGGCTGTAGATGCTGCCACTTATTACTGCCAT
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APPLICANT: Sadelain, Michel
APPLICANT: Sadelain, Michel
TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2
TITLE OF INVENTION: Antibodies
FILE REFERENCE: MSK.P-013-2
CURRENT APPLICATION NUMBER: US/10/075,947A
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 09/142,974
PRIOR APPLICATION NUMBER: 09/142,974
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1997-03-20
PRIOR FILING DATE: 1996-03-20
NUMBER: OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver: 2.1
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 3
LENGTH: 1176
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Best Local Similarity
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LOCATION: (37)
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Larson, Steven M.
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100.0%; Pr
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0; Mismatches 0;
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; SEQ ID NO 5 '
; LENGTH: 717
; TYDE: DNA
; TYDE: DNA
; ORGANISM: Homo sapiens
; PRATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(717)
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Best Local Similarity 90.1%;
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TITLE OF INVENTION: MEUROLOGICAL DISEASES AND DISORDERS
FILE REFERENCE: SOLOMON-2D
CURRENT APPLICATION NUMBER: US/09/808,037
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 09/473,653
PRIOR APPLICATION NUMBER: US 60/152,417
PRIOR APPLICATION NUMBER: US 60/152,417
PRIOR PILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
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APPLICANT: HANAN, Eilat
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                                                                                      ACTACGGTCCCGTTTGCTTACTGGGTCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGA 357
                                                                       ACTATGTCCTACTTTGACTACTGGGGCCAAGTGACCACGGTCACCGTCTCCTCAGGTGGA
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Pred. No. 2.6e-187;
0; Mismatches 68;
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RESULT 5
US-10-162-889-5
US-10-162-889-5
Sequence 5, Application US/10162889
Publication No. US20030077252A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SOLOMON, Beka
APPLICANT: HANAN, Eilat
TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME
TITLE OF INVENTION: USEFUL IN DIAGNOSING
TITLE OF INVENTION: UND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
FILE REFERENCE: SOLOMON=2B
CURRENT FILING DATE: 2002-06-06
FRIOR APPLICATION NUMBER: US/10/162,889
CURRENT FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US/09/629,971
PRIOR APPLICATION NUMBER: US/09/629,971
PRIOR APPLICATION NUMBER: US/09/629,971
PRIOR APPLICATION NUMBER: US/09/629,971
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 29
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SEQ ID NO 5
LENGTH: 717
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ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (1)..(717)
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RESULT 6 US-10-384-788-5

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Sequence 5, Application US/10384788
Publication No. US20040013647A1
GENERAL INFORMATION:
APPLICANT: SOLOMON, Beka
APPLICANT: FRENKEL, Dan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A PLAQUE-FORMING DISEASE
FILE REFERENCE: SOLOMON: 2D.
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RESULT 7

US-10-618-856-5.

Sequence 5, Application US/10618856

Publication No. US20040052766A1

GENERAL INFORMATION:

APPLICANT: SOLOMON, Beka
APPLICANT: FRENKEL, Dan

TITLE OF INVENTION : IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY

FILE REFERENCE: SOLOMON=2A

CURRENT APPLICATION NUMBER: US/10/618,856

CURRENT FILING DATE: 2003-07-15

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: US 60/152,417

PRIOR FILING DATE: 1999-03

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.0

SOFTWARE: Patentin version 3.0

SOFTWARE: CDS

NAME/KEY: CDS

LOCATION: (1)..(717)
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 Sequence 19, Application US/10259087A
publication No. US20030130190A1
GENERAL INFORMATION:
APPLICANT: Vanderbilt University
APPLICANT: Hallahan, Dennis E
APPLICANT: Qu, Shimian
TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO FILE REFERENCE: 1242/47/2
CURRENT APPLICATION NUMBER: US/10/259,087A
CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US 60/328123
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 726
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Pred. No. 2.6e-187;
0; Mismatches 68;
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RESULT 9
US-10-689-006-19
; Sequence 19, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Mernaugh, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO
; FILE REFERENCE: 1242/72
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ORGANISM: Artificial
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CURRENT APPLICATION NUMBER: US/10/689,006
CURRENT FILING DATE: 2003-10-20
PRIOR APPLICATION NUMBER: US 09/914,605
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 10/259,087
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
LENGTH: 726
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; NAME/KEY: CDS
; LOCATION: (1)..(726)
US-10-689-006-19
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Matches 635
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TYPE: DNA
ORGANISM: Artificial
PEATURE:
OTHER INFORMATION: Ar
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               CATCAGCGGAGTAGTTACCCGCTCACGTTCGGTGCTGGGACACAGTTTGGAAATAAAACGG
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Sequence 23, Application US/10689006
Publication No. US20040191249A1
GENERAL INFORMATION:
APPLICANT: Vanderbilt University
APPLICANT: Vanderbilt University
APPLICANT: Vanderbilt University
APPLICANT: Wernaugh, Raymond
TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
FILE REFERENCE: 1242/72
CURRENT APPLICATION NUMBER: US/10/689,006
CURRENT FILING DATE: 2003-10-20
PRIOR APPLICATION NUMBER: US 9/914,605
PRIOR FILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-09-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
LENGTH: 786
TYPE: DNA
ORGANISM: aftificial
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; LOCATION: (1)...(786)
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                                                                                                                 TCAAGTATAAGTTACATGCACTGGTACCAGCAGAAGCCTGTCACCTCCCCCCAAAAGATGG
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                                                 ATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCT
                                                                                               TCAAATGTAAAGTACATGTACTGGTACCAGCAGAAGTCAGGTGCCTCCCCCAAACTATGG
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                                ATTTATTACACATCCAACCTGGCTTCTGGAGTCCCAGCTCGCTTCAGTGGCAGTGGGTCT
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Pred. No. 1.3e-176;
0; Mismatches 88;
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APPLICANT: Vanderbilt University
APPLICANT: Hallahan, Dennis E
APPLICANT: Hallahan, Dennis E
APPLICANT: Qu, Shimian
TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED |
FILE REFERENCE: 1242/47/2
CURRENT APPLICATION NUMBER: US/10/259,087A
CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US 60/328123
PRIOR APPLICATION NUMBER: US 60/328123
PRIOR FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO. 17
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial
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LOCATION: (1)..(726)
OTHER INFORMATION:
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Local Similarity 86.4%;
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CCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGGCAGCTCA 477
                                   GGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATTGAGCTCACCCAGTCT
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vo. US20030130190A1
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Pred. No. 7.1e-174;
O; Mismatches 95;
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APPLICANT: Vanderbilt University
APPLICANT: Hallahan, Dennis E
APPLICANT: Hallahan, Dennis E
APPLICANT: Hallahan, Dennis E
APPLICANT: Hallahan, Dennis E
APPLICANT: Mernaugh, Raymond
TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE MEOANTIGENS
FILE REFERENCE: 1242/72
CURRENT APPLICATION NUMBER: US/10/689,006
CURRENT APPLICATION NUMBER: US 09/914,605
PRIOR APPLICATION NUMBER: US 09/914,605
PRIOR APPLICATION NUMBER: US 10/259,087
PRIOR APPLICATION NUMBER: US 10/259,087
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.2
LENGTH: 726
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US-10-689-006-17
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; LOCATION: (1)..(726)
US-10-689-006-17
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial
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                                                                                            AAGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTAC 240
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86.4%;
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Pred. No. 7.1e-174;
0; Mismatches 95;
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APPLICANT: CO1a, et al.

FILE REFERENCE: 67437-2003.1

CURRENT FILING DATE: 2003-04-07

FRIOR APPLICATION NUMBER: US/10/408,930

CURRENT FILING DATE: 2003-04-07

FRIOR APPLICATION NUMBER: PCT/AU99/00341

PRIOR FILING DATE: 1999-05-07

PRIOR PILING DATE: 1999-05-07

PRIOR PILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: AU PP3445

PRIOR FILING DATE: 1998-05-08

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin version 3.0

SEQ ID NO 4

LENGTH. 807
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                                                                                                                                                                                                                   Matches 610;
                                                                                                                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                                                                                                                        LENGTH: 807
TYPE: DNA
ORGANISM: Homo Sapeins
FEATURE:
NAME/KEY: misc feature
LOCATION: (1).-[807)
OTHER INFORMATION: Sequence of the anti-hepatitis surface antigen (4C2) scFv
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85.2%;
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                                                                                                                                                                                                                   Score 547.6; DB 16;
Pred. No. 5.5e-172;
0; Mismatches 106;
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Gaps

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121 69 61

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Sequence 1, Application US/10247488

Publication No. US20030022244A1

GENERAL INFORMATION:
APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53

FILE REFERENCE: 1196336-RAMOT
CURRENT APPLICATION NUMBER: US/10/247,488

CURRENT FILING DATE: 2002-09-20

PRIOR APPLICATION NUMBER: US/09/526,738

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US-10-247-488-1
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Best Local Similarity
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                                                                                             ICTGGCTACACCTTTACTAGCTACTGGATGAACTGGGTAAAACAGAGG
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                                                                                                                                                                                                                                                                                     Score 534.2; DB 14;
Pred. No. 1.6e-167;
0; Mismatches 105;
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FILE REFERENCE: 1196336-RAMOT
CURRENT APPLICATION NUMBER: US/10/247,488
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/526,738
PRIOR APPLICATION NUMBER: US/09/526,738
PRIOR PELICATION NUMBER: US/09/526,738
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Search completed: February 19, 2005, 02:16:16 Job time : 466.472 secs

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QV1-FT020
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RC0-GN023
MR0-G1002
MR0-B150
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AUTHORS
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Molecular Genetic and Bioinformatics Laboratory
Departament of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Bra
Tel: +55 16 39639309
Fax: +55 16 39639309
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honey bee transcriptome
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                             Nunes, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G., Maia, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F., Monesi, N., Nascimento, A.M., Peixoto, P.M.V., Silva, M.F.R., Ramos, R.G.P., Reiss, L.F.L., Dias Netto, E., Souza, S.J., Simpson, A.J.G., Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Espreafico, E.M., Espindola, F.S., Paco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and Silva, W.A., Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CK629396 872 bp mRNA linear E: AMO-AA0013-110902-011-H03 AA0013 Apis mellifera cDNA,
                                                                                                                                                                                                                          Email: wilsonjr@usp.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neoptera; Endopterygota;
Apidae; Apis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apis mellifera (honey bee)
Apis mellifera
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                                                                                                                                                                sequence was derived from to quality sequence start: 66 quality sequence stop: 625 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Apis mellifera"
/mol type="mRNA"
/strain="Africanized"
/db_xref="taxon:7460"
/dex="female, worker"
/dev stage="adult"
/clone_lib="AA0013"
                                       /clone_lib="A/
/note="Organ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:45753871
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427
437
439
 61.0%;
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BF752315
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BQ321751
BQ321310
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BF836107
 Score 437.2;
                                        whole body"
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Length 872;
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BF752315 RC3 -BN042
BQ321307 RC0-CT047
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BQ321310 RC0-CT047
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BQ321310 RC0-CT047
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BQ321309 RC0-CT047
BQ372280 RC0-CT047
BQ372280 RC0-CT047
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BQ3727280 RC0-CT047
BQ337147 QV4 HT101
B1025872 ILO-MT034
B1025872 ILO-MT034
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B1030046 ILO-MT034
B1043086 QV1-CT017
B103014086 QV1-CT017
B103014086 QV1-CT017
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B103014086 QV1-CT017
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mRNA

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RESULT 2
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Matches
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                                                                                                                                                                                                               ORGANISM
                                                                          MEDLINE
                                                                                       JOURNAL
                                                                                                                                             AUTHORS
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22217875
12230545
Contact: Foster PG
Vogler, Entomology
The Natural History Muse
Cromwell Road, London, S
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                                                                                                                                                                                                                                             601 bp carabus4g12.b Carabus granulatus carabus4g12 5', mRNA sequence. BQ474958
BQ474958.1 GI:25957232
                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae; Carabini; Carabina; Carabus; Carabus.
                                                                                                                                                                                                           Carabus granulatus
Carabus granulatus
                                                                                    Comparison of EST libraries from seven beetle framework for phylogenomics of the Coleoptera Insect Mol. Biol. 11 (5), 467-475 (2003)
                                                                                                                             Vogler, A.P.
                                                                                                                                        Theodorides, K., de Riva, A.,
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        Museum
on, SW7
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0; Mismatches 111;
        5BD
                                                                                                                                        Gomez-Zurita,J.,
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cDNA Carabus
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                                                                                                              species:
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                                 AUTHORS
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Best Local Similarity
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                                                                                                                                                                                                                                                                60
  Apidae; Apis.

1 (bases 1 to 1104)

Nunes, F.M.F., Valente, V., Sousa, J.F.,
Maia, R.M., Araujo, D.D., Costa, M.C.R.,
Monesi, N., Nascimento, A.M., Peixoto, P.
                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apo
                                                                                                 Apis mellifera (honey bee)
Apis mellifera
                                                                                                                                                     1104 bp
AM2-AA0023-091202-021-F02 AA0023
sequence.
CK629846
                                                                                                                                          CK629846.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: p.foster@nhm.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                              AGCGGAGTAGTTACCCGCTCACGTTCGGTGCTGGGACACAGTTGGAAATAAAACGG
                                                                                                                                                                                                                                                                                                                                   CTTATTCTCTCACAATCAGCAGCATGGAGGCTGTAGATGCTGCCACTTATTACTGCCATC
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                                                                                                                                                                                                                                                                                                                      CTTATTCTCTCACAATCAACCGAATGGAGGCTGAGGATGCTGCCACTTATTACTGCCAGG
                                                                                                                                                                                                                                                                                                                                                                          ACACATCCAACGTGGCTCCTGGAGTCCCTTTTCGCTTCAGTGGCAGTGGGTCTGGGACCT
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/note="Vector: pUC18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:118799'
/clone="carabus4g12"
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Pred. No. 3e-116;
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pis mellifera cI
     Cunha, M.A.V., Martins, W.K., O., Martins, W.K., O., Silva, M.
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Open reading frame ESTs - an efficient strategy for analysis of the hondy bee transcriptome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was derived from the FAPESP Genome High quality sequence start: 64 High quality sequence stop: 594.
Location/Qualifiers
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Molecular Genetic and Bioinformatics Laboratory
Departament of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Bra
Tel: +55 16 39639309
Fax: +55,16 39639309
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Unpublished (2004)
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                  CTCTTATTCTCTCACAATCAGCAGCATGGAGGCTGTAGATGCTGCCACTTATTACTGCCA 659
                                                                                          TGACACATCCAAACTGGCTTCTGGAGTCCCCTGCTTCAGTGGCAGTGGGTCTGGGAC
                                                                                                                                                                 TATAAGTTACATGCACTGGTACCAGCAGAAGCCTGTCACCTCCCCCAAAAGATGGATTTA
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                                                                                                                                             TATACGTTACATATATTGGTACCAACAGAAGCCTGGATCCTCCCCCAGACTCCTGATTTA
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CTCTTATTCTCTCACAATCAACCGAATGGAGGCTGAGGATGCTGCCACTTATTACTGCCA
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/strain="Africanized"
/db_xref="taxon:7460"
/sex="female, worker"
/dev_stage="adult"
/clone_lib="AA0023"
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Pred. No. 1.1e-114;
0; Mismatches 115;
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REFERENCE
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Contact: Silva Jr, W. A.

Molecular Genetic and Bioinformatics Laboratory
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Rua Tenente Catao Roxo, 2501, CEP 14051-140, Bra
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Fax: +55 16 39639309
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CGTCTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCTGTGGCGGTTGGCGGATCGGACAT
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/clone_lib="AA0014"
/note="Organ: whole body"
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Nunes, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G., Maia, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F., Monesi, N., Nascimento, A.M., Peixoto, P.M.V., Silva, M.F.R., Ramos, R.G.P., Reis, L.F.L., Dias Neto, E., Souza, S.J., Simpson, A.J.G., Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Espreafico, E.M., Espindola, F.S., Paco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and Silva, W.A., Jr.
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Apis mellifera
Eukaryota; Meta
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Email: wilsonjr@usp.br
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Molecular Genetic and Bioinformatics Laboratory

Molecular Genetics, FMRP/USP, FUNDHERP

Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil

Tel: +55 16 39639309

Fax: +55 16 39639309
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                                                                      Aplude; Priv.

1 (bases 1 to 672)

1 (bases 1 to 672)

Nunes, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G., Martins, W.K., Carvalho, A.F., Matia, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F., Monesi, N., Nascimento, A.M., Peixoto, P.M.V., Silva, M.F.R., Monesi, N., Nascimento, A.M., Peixoto, B., Souza, S.J., Simpson, A.J.G., Ramos, R.G.P., Reis, L.F.L., Dias Neto, B., Souza, S.J., Simpson, A.J.G., Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Espreafico, E.M., Zago, M.A., Sago, L.M., Zago, M.A., Sago, L.M., Zago, M.A., Sago, L.M., Zago, M.A., Sago, M.A., Sago, L.M., Zago, M.A., Sago, L.M., Zago, M.A., Sago, L.M., Zago, M.A., Sago, M.A., Sago, L.M., Zago, M.A., Sago, L.M., Zago, M.A., Sago, L.M., Zago, M.A., Sago, L.M., Zago, M.A., Sago, M.A., S
Open reading frame ESTs -
honey bee transcriptome
Unpublished (2004)
                                                                  Espindola, F.S., Paco-Larson, M.L., Silva, W.A. Jr.
                                                                                                                                                                                                                             Apidae; Apis.
1 (bases 1 +
                                                                                                                                                                                                                                                               Apis mellifera (honey bee)
Apis mellifera
Eukaryota, Metazoa, Arthropoda, Hexap
Neoptera, Endopterygota, Hymenoptera,
                                                                                                                                                                                                                                                                                                                                                          CK633068.1
EST.
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Pred. No. 8.2e-111;
0; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                            672 bp mRN
AP0011 Apis
                                             an
                                           efficient strategy
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ptera; Apocrita; Aculeata; Apoidea;
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                                                        DEFINITION
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Matches 480; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296
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Tel: +55 16 39639309
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Email: wilsonjr@usp.br
This sequence was derived from the FAPESD Ganoma Decrease.
sequence.
                                                        CK633069 672 bp mRNA linear E. AM3-AP0011-070602-021-A08 AP0011 Apis mellifera cDNA,
                                                                                                                                                                                                                                                                 ATGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGC 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGGTGAAACTGCAGCAGTCA-GGACCTGAACTGGTGNAGCC-TGGGGCTTCAGTGAAGA
                                                                                                                                                                                                                                                                                                                                                                               CAGCTCAAGTATAAGTTACATGCACTGGTACCAGCAGAAGCCTGTCACCTCCCCCAAAAG 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATACAATGAGAAGTTCAAGGGCAGGGCCACACTGAGTGTAGACAAGTCCTCCAGCACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGTGAAGCTGCAGCAGTGAGGGAACAGAAGTGGTAAAAGCCGTGGGGCTTCAGCTGAAG 13 6
                                                                                                                                                                                                                                CCTGATTTATGACACATCCAACGTGGCTCCTGGAGTCCCATTTCGCTTCAGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGG 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTACAAGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGC 236
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                                                                                                                                                                                                                                                                                                                                              CAGCTCAAGTATACGTTACATATATTGGTACCAACAGAAGCCTGGATCCTCCCCCAGACT
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/db xref="taxon:7460"
/sex="female, worker"
/dev stage="pupal"
/clone_lib="AP0011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Organ: whole body"
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80.7%;
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AUTHORS
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Apis mellifera
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This sequence was derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rua Tenente Catao Roxo,
Tel: +55 16 39639300
Fax: +55 16 39639309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silva, W.A. Jr.
Open reading frame ESTs
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Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apo
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                                                                                         AGGTGGAGGCGGTTCAGGCGAGGTGGCTCTCGGCGGTGGCGGATCGGACATCGAGCTCAC 410
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     TCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGG
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/dev_stage="pupal"
/clone_lib="AP0011"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="Africanized"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Apis mellifera"
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Pred. No. 1.9e
0; Mismatches
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1.9e-97;
nes 105;
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REFERENCE
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SOURCE
ORGANISM
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                                                                                                                                                                                                 166
                                                                                                                                                                                                                                       460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Silva Jr, W. A.

Molecular Genetic and Bioinformatics Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nunes, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G., Maia, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F., Monesi, N., Nascimento, A.M., Peixotto, P.M.V., Silva, M.F.R., Ramos, R.G.P., Reis, L.F.L. Dias Neto, E., Souza, S.J., Simpson, A.J.G., Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Espreafico, E.M., Espindol, F.S., Paco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and
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CK629843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: wilsonjr@usp.br
This sequence was deriv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       honey bee transcriptome Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apis mellifera
Apis mellifera
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AM2-AA0023-091202-021-H05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Silva, W.A. Jr.
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Nunes, F.M.F., Valente, V.,
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Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apo
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                                                                                                                                                                                                                                                       Similarity
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                               CTGTGCAAGAG-----ATACTACGGTCCCGTTTGCTTACTGGGTCCAAGGGACCAC-G
                                                                                                                                                         GGGGATGCTGAGTACAATGAGAA-TTCAATGGCAGGGCCACACTGAGTGTAGACAAGTCC
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                                                                               TCCAGCACAGCCTATATGGAGCTCACTAGGCTGACATCTGAGGACTCTGCTGTCTATTTG
                                                                                                       TCCAGCACAGCCTACATGGAGCTCCGCAGCCTGACATCTGAGGATTCTGCAGTCTA-TTA
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       CTGTGCTAGAGGGGACTACTATAGGCGCTACTTTGACTTGTGGGGGCTCAAGGGACCACGG
                                                                                                                                                                                           GGTGGTACTAACTACAAGCAGAAGTTCAAGGGCCAAGGCCACATTGACTGTAGACAAGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence start: 88 quality sequence stop: 376.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence was derived from
                                                                                                                                                                                                                                     48.1%;
llarity 82.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Apis mellifera"
/mol_type="mRNA"
/strain="Africanized"
                                                                                                                                                                                                                                                                                                                                   /note="Organ: whole body"
                                                                                                                                                                                                                                                                                                                                                   sex="female, worker"
dev_stage="adult"
clone_lib="AA0023"
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                                                                                                                                                                                                                                                                                                                                                                                                           xref="taxon:7460"
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                                                                                                                                                                                                                                   Score 344.6; DB Pred. No. 2e-90; 0; Mismatches
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Apis mellifera cDNA, mRNA
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                                                                                                                                                                                                                                                                         Length
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AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                     Molecular Genetic and Bioinformatics Laboratory Departament of Genetics, FMRP/USP, FUNDHERP Rua Tenente Catao Roxo, 2501, CEP 14051-140, Bra Tel: +55 16 39639309
Fax: +55 16 39639309
Email: wilancia
                                                                                                                                                                                                                                                                                                                                                                                                                         Nunes, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G., Maia, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F., Monesi, N., Nascimento, A.M., Peixoto, P.M.V., Silva, M.F.R., Ramos, R.G.P., Reis, L.F.L., Dias Neto, E., Souza, S.J., Simpson, A.J.G., Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Espraefico, E.M., Espindola, F.S., Paco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and Silva, W.A. Jr.
                                                                                                                                                   Email: wilsonjr@usp.br
This sequence was derived from the
High quality.sequence start: 70
High quality sequence stop: 545.
Location/Qualifiers
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CK632348
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/sex="female, worker"
/dev_stage="Mix of adult,
/clone_lib="AM0009"
                                                                               /mol_type="mRNA"
/strain="Africanized"
                                                                                                                 organism="Apis mellifera"
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                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 567)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. A
                                                                                                                                                                                                          Homo sapiens
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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10737800
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This sequence was derived from the FAPESP/LICR Human Cancer Genome

This sequence was derived from the following URL

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-RT0048-
210201-003-e06&t3=2001-02-21&t4=1)

Seq primer: puc 18 forward.
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                                                                           GCTGCCACTTATTACTGCCATCAGCGGAGTAGTTACCCGCTCACGTTCGGTGCTGGGACA
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                                                                                                                                            AGTGGCAGTGGGTCTGGGGACCTCTTATTCTCTCACAATCAGCAGCATGGAGGCTGTAGAT
                                                                                                                                                                                                               TCCCCCAAAAGATGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTTC
                                                       GCTGCCACTTATTACT-CCAGGAGTGGAGTGGTTATCC-TACACTTTCGGAGGGGGGACA
                                                                                                                          AGTGGCAGTGGGTCTGGGACCTCTTATTCTCTCACAATCAACCGAATGGAGGCTGAGGAT
                                                                                                                                                                                           TCCCCCAGACTCCTGATTTATGACACATCCAACGTGGCTCCTGGAGTCCCTTTTCGCTTC
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//note="Organ: kidney_tumor; Vector: puc18; Site_1: SmaI;
/note="Organ: kidney_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
law stringency conditions."
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mol type="mRNA"
/db xref="taxon:9606"
/dev stage="Adult"
/clone_lib="RT0048"
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Pred. No. 4.6e-88;
0; Mismatches 91;
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ILO&t2=ILO-MT0355-
220301-500-dll&t3=2001-03-22&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maumalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 585)

Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Dias Neto, E., García Correa, R., Verjovski-Almeida, Costa, F.F., Dasai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
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High quality sequence star!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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                                     GCTCACTCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="MT0355"
/note="Organ: marrow; Vector: pucl8; Site_1: SmaI; Site_2: fnote="Organ: marrow; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                    Score 329.4; DB 4;
Pred. No. 5.5e-86;
D; Mismatches 81;
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SOURCE
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1 (bases 1 to 476)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV4&t2=QV4-NT0248-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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QV4-NT0248-271100-585-c10 NT0248 Homo
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Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
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/CLORE 11b="NT0248"
/CLORE 11b="NT0248"
/CLORE 12b="NT0248"
/NOTE="Organ: nervous tumor; Vector: puc18; Site_1: SmaI;
/NOTE="Organ: nervous tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORSGTES PCR (U.S. Letters Patent application
NO. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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1 (bases 1 to 498)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Ragai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
                                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QVI&t2=QVI-FT0202-
071100-465-903&t3=2000-11-07&t4=1)
                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF897861
QV1-FT0202-071100-465-g03
BF857861
Seq primer: puc 18 forward High quality sequence start: 8 High quality sequence stop: 497
                                                                                                                                             Rua Prof. Antonio Prudente 109,
Brazil
                                                                                                                                 Tel: +55-11-2704922
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Matsukuma, A., Baia, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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QV1-FT0202-071100-465-f03
                                               Shotgun sequencing of the human transcriptome with ORF
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Mammalia; Eutheria;
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llarity 87.0%;
Conservative
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/do_xref="taxon:9606"
/do_bref="taxon:9606"
/do_bref="caxon:9606"
/do_bref="caxon:9606"
/do_bref="caxon:9606"
/clone_lib="FT0202"
/clone_lib="FT0202"
/note="Organ: prostate_tumor; Vector: pucl8; Site_1: Smal;
/note="Gram1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
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Pred. No. 5.6e-82;
0; Mismatches 52;
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3 FT0202
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Simpson A.J

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DEFINITION
ACCESSION
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QV1-FT0170-040700-265-b10
BQ373705
BQ373705.1 GI:21049219
EST.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2=QV1-FT0202-
071100-465-f03&t3=2000-11-07&t4=1)
Seq.primer: puc 18 forward
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
Brazil
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                   Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-2704922
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lb_xref="taxon:9606"

lev_stage="Adult"

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Pred. No. 3.7e-81;
0; Mismatches 50
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FT0170 Homo sapiens
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REFERENCE
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1 (bases 1 to 427)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@lidwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QVI&t2=QV1-FT0170-
040700-265-b10&t3=2000-07-04&t4=1)
Seq.primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer R
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CTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTATTCTCTCACAATCAGCAGCATGGAGG
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                                                                                                                                                                                                       TCACCATGACCTGCAGTGGCAGCTCAAGTATAAGTTACATGCACTGGTACCAGCAGAAGC
                                                                            CTGGATCCTCCCCAGACTCCTGATTTATGACACATCCAACGTGGCTCCTGGAGTCCCTT
                                                                                                       CTGTCACCTCCCCCAAAAGATGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTG
                                                                                                                                                                     TCACCATGACCTGCAGTGCCAGCTCAAGTATACGTTACATATATTGGTACCAACAGAAGC
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/mol type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0170"
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Location/Qualifiers
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Copyright (c) 1993 - 2005 Compugen Ltd.
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310.8	312.8	312.8	312.8	313.4	314.8	317.2	317.2	318	318	323.6	336.6	336.6	347	351	351	352.6	383.2	393.2	393.2	393.2	393.6	394.8	396.2	396.2	398.2
43.5	43.8	43.8	43.8	43.9	44.1	44.4	44.4	44.5	44.5	45.3	47.1	47.1	48.6	49.2	49.2	49.4	53.7	55.1	55.1	55.1	55.1	55.3	55.5	55.5	55.8
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M36217 Mouse Ig he	AX363235 Sequence	AX363234 Sequence	AX363232 Sequence	AY648611 Mus muscu	M76414 Mouse IgM c	AY648617 Mus muscu	AY648618 Mus muscu	AR365720 Sequence		M36228 Mouse Ig he	AX023355 Sequence	BD222932 Heteromin	AJ564232 Synthetic	M69273 Cloning vec	M69286 Recombinant	L43544 Mus musculu	AX590282 Sequence	AR306901 Sequence	BD226888 Improveme	A95266 Sequence 12	AR364986 Sequence	AR343614 Sequence	I45910 Sequence 6	E07990 DNA encodin	AR154831 Sequence

ALIGNMENTS

DЪ	γQ	Db	Qy	DЪ	Q	Db	φ	Query Match Best Local Matches 71	ORIĢIN	Bource	JOURNAL		TITLE	REFERENCE		ORGANISM	KEYWORDS	VERSION	ACCESSION	LOCUS	RESULT 1 AR231455
181 CGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCT	181 CGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCT	121 GGCAGTCTCCGAAACTGCTGATATACTCTGCATCCAATCGCTACACTGGAGTCCCTGAT	121 GGGCAGTCTCCGAAACTGCTGATATACTCTGCATCCAATCGCTACACTGGAGTCCCTGAT	61 ATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTGGCTTGGTACCAACAGAAGCCA	61 ATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTGGCTTGGTACCAACAGAAGCCA	1 AGTATTGTGATGACCCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACC	1 AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACC	Query Match 100.0%; Score 714; DB 6; Length 714; Best Local Similarity 100.0%; Pred. No. 9.1e-179; Matches 714; Conservative 0; Mismatches 0; Indels 0; Gaps	/organism="unknown" /mol_type="genomic DNA"	1714	c	anti-ganglioside GD2 antibodies, cells expressing same and related methods	Single chain FV polynucleotide or peptide constructs of	1 (bases 1 to 714)	Unclassified.	Inknown.		AR231455.1 GI:27272557	AR231455	o from latement III	
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1 (bases 1 to 1173)

Cheung, N.-K. V., Larson, S.M., Guo, H.-F., Rivlin, K. and Sadelain, M. Single chain FV polymucleotide or peptide constructs of Single chain FV polymucleotide or peptide constructs of anti-ganglioside GD2 antibodies, cells expressing same and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methods
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  CGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCT
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/organism="unknown"
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OS Mus mus
PN JP 2002
PD 16-JUL-
PF 28-JUL-
PR 28-JUL-
PR 28-JUL-
PR 28-JUL-
PR C12N15/
PC C12N5/1
PC C12N5/1
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PC (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 1371)
Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.
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BD222935
BD222935.1 GI:33032705
JP 2002521053-A/29.
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                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Mus musculus (mouse)
D 2002521053-A/29
16-JUL-2002
28-JUL-1999 JP 2000562401
28-JUL-1998 EP 98114082.5
PETER KUFER, TORSTEN DREIER, PATRICK A BAEUERLE, KATRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens (human)
                                                                                                                                        C12N5/10, C12P21/02, G01N33/53, G01N33/53//(C12N5/10, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00, A61K37/02, A61K37/66, (C12N5/00, C12R1:91)
Heterominibodies
                                                                                                                                                                                                    FLORIAN ZETTL
C12N15/09, A61K35/76, A61K38/00, A61K38/21, A61P35/00, A61P35/02, C12N15/09, A61K35/76, A61K38/00, A61K38/21, A61P35/00, A61P35/02, C07K19/00, C12R1:91), C12N5/10, C12P21/02, G01N33/53/, G01N33/53/, (C12N5/10, C12R1:91),
                                                             Location/Qualifiers
1. .1371
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                    Location/Qualifiers (10). .(1359).
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Heterominibodies
Patent: WO 0006605-A 30 10-FEB-2000;
KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER 'BAEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE)
BIOMEDIZINIS (DE)
                                                                                             Homo sapiens
Eukaryota; M
                                                            Kufer, P.,
                                                                                    Mammalia;
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                                                                                   Eutheria;
                                                         Zettl, F., Dreier, T.,
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                                                                                                                        (human)
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                                                                                  Chordata; Primates;
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Pred. No. 4.8e-116;
0; Mismatches 115;
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WO0006605.
                                                                                Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                            Baeuerle, P.A.
                                                                                                                                                                                     DNA
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                                                            Borschert, K.
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                                                                          CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTGCCAGTCGGGG
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/protein_id="CAC08832.1"
/db_xref="G1:10183772"
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ASYFCQQYNSYPLTFGAGTKLEIKGGGGSGGGGSQVKLQESGPGLVQPSQSLS
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ITCTVSGFSLTSYGVHXQSGKGLEBLLKHLGTKGGGGAPAPTSSSTKKTQLQLEHLLLDLQMIL
KHKELLKGPRKGELEBLLKHLKELLKGGSGGAPAPTSSSTKKTQLQLEHLLLDLQMIL
MGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEBELKFLEEVLNLAQSKWFHLRPR
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Pred. No. 4.8e-116;
0; Mismatches 115;
               TTTGCTTACTGGGGCCAAGGGACCACGGTCACCGTCTCC
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MICROMET AG

OS Homo sapiens (human)

OS Mus muscullus (mouse)

PN JP 2002521053-A/30

PD 16-JUL-1999 JP 2000562401

PR 28-JUL-1999 EP 98114082.5

PI PETER KUPER, TORSTEN DREIER, PATRICK A

BORSCHERT,

PI FLORIAN ZETTL

PC C12N15/09, A61K35/76, A61K38/00, A61K38/

PC C12N5/10, C12P21/02, G01N33/53, G01N33/5

PC (C12N5/10, C12P21/02, G01N33/53, G01N33/5)
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JP 2002521053-A/30.
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Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K.
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Mammalia; Eutheria; Primates;
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                                      GACCAAGCTGGAAATAAAAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCCGCTGGCGG
                                                                                                                                                                                               AGACTTGGCAGAGTATTTCTGTCAGCAATATAACAGCTATCCGCTCACGTTCGGTGCTGG
                                                                                                                                                                                                                                                AGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCT-----
                                                                                                                                                                                                                                                                                                                                                                                                 GCAATCTCCTAAAGCACTGATTTACTCGGCATCCTACCGGTACAGTGGAGTCCCTGATCG
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TTCTCAGGTGAAACTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTC
                                                                                               CTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCTGA
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C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,
C07K19/00,
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28-JUL-1998 EP 98114082.5
PETER KUPER,TORSTEN DREIER,PATRICK A BAEUERLE,KATRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 4.8e-116;
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                                                                     63 AACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTGGCTTGGTACCAACAGAAGCCAGG
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                                                                                                                                  3 TATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACCAT
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KUFER PETER (DE); ZETTL FLORIAN (DE); DRE
BAEUERLE PATRICK A (DE); BORSCHERT KATRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, F
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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 GCAGTCTCCGAAACTGCTGATATACTCTGCATCCAATCGCTACACTGGAGTCCCTGATCG
                                                                                                             TATCCAGCTGACCCAGTCTCAAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGT
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                                                                                                                                                                                   Conservative
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FHLRFRDLISNINVIVLELKGSBTTFMCEYADETATIVEFLNRWITFCQSIISTLTDV
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/mol type="unassigned DN?
/db_xref="taxon:9606"
10._.1380
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Pred. No. 4.8e-116;
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AACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTGGCTTGGTACCAACAGAAGCCAGG
                                TATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACACGGGTTACCAT
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                                                                                                                                                                                                                                           sequences; artificial sequences
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WO 2004069876-A 19
                                                                                                                                                                                          AG (DE)
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/mb.e="scFv antiEpCAM-hu4-1BBL nucleic
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1. .1380
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                                         GGGTAACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTC
                                                                                       CTTTAAAATGAACAGTCTGCAAGCTAATGACACAGCCATATATTACTGTGCCAGAATGG-
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MUSVKLI
738 bp DNA linear ROD 14-DEC-1995
Mus musculus (clone H11) Ig kappa light chain V region (Vk), Ig
heavy chain V region (Vh), and single chain FV gene.

; Ig)

kappa ; catalytic

Eukaryota; Metazoa; Chordata; Craniata; Ver Mammalia; Eutheria; Rodentia; Sciurognathi; 1 (bases 1 to 738) Suckling.C.J., Stimson,W.H., Proctor,G.R., Khalaf,A.L. and Tedford,C.M. Catalytic Antibodies - Designed and Acciden Catalytic Antibodies - Designed and Acciden Chases Soc. Perkin Trans. 1 (22), 2777-27 L41689.1 GI:1119223
Diels-Alder reaction; Ig heavy chain variable region;
light chain; Ig light chain variable region; antigen I
antibody; immunoglobulin.
Mus musculus musculus (eastern European house mouse)
Mus musculus musculus Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Accidental 2777-2780

Bence, L.H.,

Biochem. Soc. Trans. 24, 313 (1996) Original source text: Mus musculus (strain NZB x BALB/c, sub_species musculus) (clone: H1) male adult splenocyte DNP Single chain Fv constructed from an IgG1 antibody which has own to catalyse a Diels Alder Cycloaddition reaction. 2 (bases 1 to 738) Brooks, L., Suckling, C.J. and Stimson, W.H. Construction of a single chain Fv from an Diels Alder reaction antibody catalysing DNA

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Location/Qualifiers

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Query Match
Best Local S
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    TCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTG
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                                                                AGAAACCAGGGCAGTCTCCTAAGCTGCTGATCTACTGGGCATCCACTAGGGAATCTGGTG
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391. .732
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GYGYNMVRQPPGKGLEMIGMIMGDGNTDYNSALKSRLSISKDNSKSQVFLKYMNSLHTD
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/note="This CDS feature is included to show the
/note="This CDS feature is included to show the
/ranslation of the corresponding V region. Presently
translation qualifiers on V_region_features are illegal."
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/product="Ig heavy chain variable region"
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/standard name="Vk linker VH"
/note="linked by a flexible bridging
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/dev_stage="adult"
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L_type="hybridoma"
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Pred. No. 8.6e-104;
0; Mismatches 115;
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Submitted (07-MAY-1997) Dept.
Agricultural University, P.O.
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                                                                                                                                                                                                                                                                                                                                                    Schouten,A., Roosien,J., de Boer,J.M., Wilmink,A., Rosso,M.N., Bosch,D., Stiekema,W.J., Gommers,F.J., Bakker,J. and Schots,A. Improving scFv antibody expression levels in the plant cytosol PEBS Lett. 415 (2), 235-241 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 840)
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840 bp mRNA musculus mRNA for IgM/kappa antibody,
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                                                                                                                                                                                                                                                                                              (bases 1 to 840)
/codon_start=1
/product="IgM/kappa antibody"
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                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                              Location/Qualifiers
                                                                                'db_xref="taxon:10090"
'note="recombinant gen
                                                                .840
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Box 8123, Wageningen 6700
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  TACTGTGCCAAAAATTACTATGGTAACTACGGGGCTATGGACTACTGGGGTCAAGGAACC
                                              TCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTAC
                                                                                                        GGTGGAAGCACAAATTATAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAACGACCAAC
                                                                                                                                                    GTACACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCT
                                                                                                                                                                                                  CGCTCACAGAGCCTGTCCAATCACTTGCACTGTCTCTGGGTTTTTCATTAACCAATTATGGT
                                                                                                                                                                                                                                                TCTG----GCGGTGGCGGATCGCAGGTGCAGGTGAAGGAGTCAGGACCTGGCCCTGGTGGCG
                                                                                                                                                                                                                                                                                                                                                                             TACCAACAGAAGCCAGGGCAGTCTCCGAAACTGCTGATATACTCTGCATCCAATCGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACCATA
               TACTGTGCCAGTCGGGGGGTAACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACC
                                                                                                                                         GTACACTGGG
                                                                                                                                                                                     CCCTCACAGAGCCTGTCCATAACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGT
                                                                                                                                                                                                                                                                                 ACGTTCGGTGCGGGACCAAGCTGGAAATAAAACGGGAGGGTAAATCCTCAGGATCTGGC
                                                                                                                                                                                                                                                                                                                              AGCAGTGTACAAGCTGAAGACCTGGCAGTTTATTACTGTCATCAATACCTCTCCTCGCTC
                                                                                                                                                                                                                                                                                                                                             AGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCGC--
                                                                                                                                                                                                                                                                                                                                                                                                                           TACCAGCAGAAACCAGGCAGTCTCCTAAACTGCTGATCTACTGGGCTTCCACTAGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTGCAAGGCCAGTCAGAGTGT------GAGTAATGATGTGGCTTGG
                                                                                           GGTGGAAGCACAGACTACAATGCAGCTTTCATGTCCAGACTGAGCATCACCAAGGACAAC
                                                                                                                                                                                                                                    TCCGAATCCAAACTCGAGTCTGAGGTGAACCTGGTGGAATCTGGACCTGGCCTAGTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Heavy chain ! coding sequence" 787. .819 /note="c-myc tag code 826. .837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Light chain var
355. .402
/note="Linker peptide
403. .759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MAQVDGDIQMTQSPPSLAVSAGEKVTMSCKSSQSVLYSSNQKNY LAWYQQKFGGSFKLLIYMASTRESGVBPRFTGSGSGTDFTLTISVQAEDLAVTYCHQ YLSSLTFGAGTKLEIKREGKSSGSGSESKLESEVNLVESGFGLVQPSQGELSITCTVSG FSLTSYGVHWYRQSPGKLEWLGVIWRGGSTDYNAAFMSRLSITKDNSKSQVFFKMNS LQADDTAIYYCAKNYYGNYGAMDYWGQGTSVTVSAPKTTPGAAAEQKLISEEDLNDIK
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76.3%;
                                                                                                                                         CGCCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 417.2; DB 10;
Pred. No. 7.3e-100;
0; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain variable
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AUTHORS
TITLE
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FEATURES
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Sequence 31
AR481833
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Location/Qualifiers
1, .752
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Ledbetter, J.A., Hayden, M., Fell, P., Mittler, R.
Modified sFv molecules which mediate adhesion !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uses thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown.
                                                                                                                            CTCGGAGGGGGGACCAAGCTGGAAATAAAA---GGTGGAGGCGGTTCAGGCGGAGGTGGC
                                                                                                                                                                                                                                                                                 GTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGC-----AGGATTATAGCTCG
                                                                                                                                                                                                                                                                                                                                 GTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACT
                                                                                                                                                                                                                                                                                                                                                                               CAGAAGCCAGGGCAGTCTCCGAAACTGCTGATATACTCTGCATCCAATCGCTACACTGGA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACACGGGTTACCATA
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AAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTAC
                                                GGAAGCACAAATTATAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACAACTCC
                                                                                             CACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGT
                                                                                                                                                                                                                                                                                                                     CAGAAACCAGGACAGCCAAACTCCTCATCTCTGCTGCATCCAACGTAGAATCTGGG
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                                    GGAAGCACAGACTATAATTCAGCTCTCAAATCCAGACTGAGCATCACCAAGGACAACTCC
                                                                                AACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAATGATATGGGGTGAT
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ilarity 76.9%;
Conservative
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Pred. No. 4.1e-99;
0; Mismatches 141;
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TITLE
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Best Local Similarity
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Sequence
AR481832
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Ledbetter, J.A., Hayden, M., Fell, P., Mittler, R.
Modified sFv molecules which mediate adhesion b
uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent: US 6699715-A 30 02-MAR-2004;
Location/Qualifiers
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Unclassified.
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                                       CACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGTGATGACCCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACCATA
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 GGAAGCACAAATTATAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACAACTCC
                        AACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAATGATATGGGGGTGAT
                                                                                         TCACAGAGCCTGTCCATCACTTGCACTGTCTCTGGGTTTTTCATTAACCAATTATGGTGTA
                                                                                                                           TCGGGTGGCGGATCTCAGGTGCAGCTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCC
                                                                                                                                        TCTGGCGGTGGCGGATCGCAGGTGCAGGTGAAGGACTCAGGACCTGGCCCTGGTGGCGCCC
                                                                                                                                                                           TTCGGTGGAGGCACCAAGCTGGAAATCAAACGGGGTGGCGGGGGGCGCTGGTGGG
                                                                                                                                                                                           CTCGGAGGGGGACCAAGCTGGAAATAAAA----GGTGGAGGCGGTTCAGGCGGAGGTGGC
                                                                                                                                                                                                                            GTGGAGGAGGATGATATTGCAATGTATTTCTGTCAGCAAAGTAGGAAGGTTCCTTGGACG
                                                                                                                                                                                                                                           GTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGC------AGGATTATAGCTCG
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                                                                          TCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTCTCATTAACCGGCTATGGTGTA
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/mol_type="genomic DNA"
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76.9%;
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Pred. No. 3.9e-99;
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    and Winberg,
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ORGANISM
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AR481831
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Unknown.
Unclassified.
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Location/Qualifiers
1. .1527
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Ledbetter,JA., Hayden,M., Fell,P., Mittler,R.
Modified sFv molecules which mediate adhesion
uses thereof
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                          TCACAGAGCCTGTCCATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGGTGTA
                                                              TTCGGTGGAGGCACCAAGCTGGAAATCAAACGGGGTGGCGGTGGCTCGGGGGGGTGGTGG
                                                                                                                                       CTCGGAGGGGGACCAAGCTGGAAATAAAA---GGTGGAGGCGGTTCAGGCGGAGGTGGC
                                                                                                                                                                GTGGAGGAGGATGATATTGCAATGTATTTCTGTCAGCAAAGTAGGAAGGTTCCTTGGACG
                                                                                                                                                                              GTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGC------AGGATTATAGCTCG
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/mol_type="genomic
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Pred. No. 3.9e-99;
0; Mismatches 141
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Sequence
AR364987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 729)
Ladner, R.C., Bird, R.E. and Hardman, K.
Ladner, Brid, R.E. and Hardman, K.
Immunotheraphy using single chain polypeptide
Pateint: US 5455030-A 16 03-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unclassified.
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                               TCGCAGGTGCAGGTGAAGGAGTCAGGACCTGGCCCTGGTGGCGCCCCTCACAGAGCCTGTCC 414
                                                                                                  ACCAAGCTGGAAATAAAAAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGA
                                                                                                                                                          GAAGACCTGGCAGTTTATTTCTGTCAGCAG-----GATTATAGCTCGCTCGGAGGGGGG
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               CTGGATGTGCAGCTGAAGGAGTCAGGACCTGTCCTGGTGGCGCCCTCACAGAGCCTGTCC
                                                                                                                                     GAAGATGCTGCCACTTATTACTGTCAGCAGTACAGTGGTTACGGACTCACGTTCGGTGCT
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                                                                          CCCACCAAGCTTAAAGAATCTGGTTCTGTTTCTTCTGAACAGCTGGCTCAGTTTCGTTCT
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/mol_type="genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Pred. No. 1.8e-97;
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Produktion und Charakterisierung supra-agonistischer bispezifischer CD28-Antikoerper zur Tumor-Immuntherapie
Thesis (2002) Department of Biology, University of Tuebingen,
                                                                                                                                                                                                                                                                                                                                                                                 Submitted (28-AUG-2002) Grosse-Hovest L., Max-Planck-Institute for Biochemistry, Am
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Martinsried, GERMANY
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/organism="Mus musculus"
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/db xref="taxon:10090"
/cell line="hybridoma 9.2.
1264. ..1599
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                   TCACAGAGCCTGTCCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGGTGTA
                                                                    TCTGGCGGTGGCGGATCGCAGGTGCAGGTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCC
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/db_xref="di-CD28 and anti-HMWG ScFv antibody"
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SQSLSITCTVSGFSLSDYGYHWVRQSPEQGLEWLGYIWAGGGTTVTVSSALMSRKSISKD
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LAPSSSGSGQVKLQSGSPELVKPGASVTISCRASGYAFSRMNMVKQRPEQGLEWIG
RIYPGGDTNYNGKFKGKATITADKSSSTAYMQVSSLTSVDSAVYFCARGNTVVVPYT
MDYWGQGTTVTVSSGGGGSGGGGSGGGGSGDIELTQSPASLAVSLGQRATISCRASSSV
DSYGNSFMHWYQQKFGQPFKLLIYLASNLESGVPARFSGSGSRTDFTLTIDPVEADDA
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/db_xref="taxon:10090"
/cell_line="hybridoma'
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Ledbetter, J.A., Hayden, M., Fell, P., Mittler, R. and Winberg,
Modified sFv molecules which mediate adhesion between cells
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                        | GGTGGCTCTGGCGGTGGCGGATCG-----CAGGTGCAGGTGAAGGAGTCAGGACCTGGC
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/mol_type="genomic |
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AAZ50585

M79scFv-i

The present sequence encodes a recombinant single chain peptide, 3G6-scFv. The peptide is an antibody construct comprising the variable regions of the heavy and light chains of an antibody against disialoganglioside (GD2) as a single chain Fv fragment (scFv). GD2 occu in many tumours types including neuroblastoma, osteosarcomas and other soft tissue sarcomas, medulloblastomas, high grade astrocytomas,

GD2 occurs

toxins, to such cells.

Disclosure; Page 11-12; 31pp; English.

Recombinant single chain anti-disialoganglioside GD2 antibody - useful to detect tumour cells expressing GD2 and to target therapeutic agents, e.g.

45	44	43	42	41	40	9	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
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ALIGNMENTS

RESULT 1 AAT86310

AAT86310 standard; DNA;

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tissue imaging; target delivery; toxin; streptavidin;
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Best Local
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              Anti-disialoganglioside
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the construction of the present 366 serv gene using a mouse serv module/recombinant phage antibody system. The serv was used in fusion proteins of the invention which comprised the serv inked to the human T cell surface receptor CD28. T cells expressing such fusion proteins exhibit enhanced survival when reintroduced to an in vivo environment. They can be used to induce an immune response to cells that express the antigen to which the antibody is specific. Cells expressing a fusion protein including an anti-GD2 serv are useful for treatment of melanomas, neuroblastomas, small lung carcinoma, sarcomas and brain tumours that express GD2 as a surface antigen. Cells expressing the fusion proteins of the invention can also be used for in vitro purging of steem cells or bone bearing cells for imaging
                                                                                                                                                                                                                                                                   The present sequence is that of cDNA encoding a single chain scFv antibody that is derived from an anti-disialoganglioside GD2 antibody produced by 3G6 hybridoma cells. The scFv comprises the 3G6 variable chains in VL-VH orientation. mRNA from 3G6 hybridoma cells was used in
                                                                                                                                                                                                                                                                                                                                                                                             New fusion protein, useful for inducing host immune response, comprises variable region of light chain of an antibody linked to variable region of antibody, CD28 receptor signaling domain and transmembrane domain.
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Sequence 714 BP; 174 A; 168 C; 205
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  Recombinant single chain anti-disialoganglioside GD2 antibody - useful to detect tumour cells expressing GD2 and to target therapeutic agents, e.g.
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                            TACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
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Pred. No. 8.1e-198;
); Mismatches 0;
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                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                   The invention relates to a novel polypeptide construct comprising at least one CDR3 region comprising at least one mutation in a fully defir sequence of 6 amino acids. A construct of the invention has antiinflammatory, antimicrobial, cytostatic, immunomodulator, and immunosuppressive activity. The polypeptide construct, polynucleotide, vector or composition are useful for the prevention, treatment or amelioration of a proliferative disease, a tumorous disease, an inflammatory disease, an immunological disorder, an autoimmune disease an infectious disease in a human subject. The present sequence encodes bispecific single chain antibody scFv EpCAMxCD3 with the M1 mutant
                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2002; 2002CA-02403313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator; immunosuppressive; proliferative disease; tumour; inflammatory diseimmunological disorder; autoimmune disease; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADQ91081 standard; DNA; 1479
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       123
                                                                                                                                                                               587;
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                                                                                                                                            ω
                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ91080.
                                                                                                                                                                                                                                                     1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      construct, useful in treating, comprises at least one mutated
   GCAGTCTCCGAAACTGCTGATATACTCTGCATCCAATCGCTACACTGGAGTCCCTGATCG
                                                                                                                              TATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACCAT
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                                    CACCTGCAAGGCCAGTCAGAATGTGGGTACTAATGTAGCCTGGTATCAACAGAAACCAGG
                                                                       AACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTGGCTTGGTACCAACAGAAGCCAGG
                                                                                                          TATCCAGCTGACCCAGTCTCAAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGT
                                                                                                                                                                                                                                                                                        single chain antibody scFv the anti CD3 region.
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                 BP; 385 A; 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "scFv EpCAMxCD3 region"
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1. .1479
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                                                                                                                                                                                              67.2%;
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                                                                                                                                                                                                                                                                                      region.
                                                                                                                                                                             Score 480; DB 12;
Pred. No. 1.9e-129;
0; Mismatches 115;
                                                                                                                                                                                                                                                 C; 389 G;
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   11-OCT-2002; 2002CA-02403313
                                    11-OCT-2002; 2002CA-02403313
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CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator; immunosuppressive; proliferative disease; tumour; inflammatory disease; immunological diseader; autoimmune disease; infectious disease; scrv EpCAMxCD3; antibody; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                EpCAMxCD3 with M11 mutant
                          /*tag= a
/product= "scFv EpCAMxCD3 with M11 mutant in
region"
/note= "No start codon"
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CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTGCCAGTCGGGG
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                                                                                                         TAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTT
                                                                                                                                                                                              GCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGTGGAAGCACAAATTA
                                                                                                                                                                                                                                         CATCACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCGCCA
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Pred. No. 1.9e-129;
0; Mismatches 115;
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TATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACCAT

Query Match Best Local S Matches 587

al Similarity 587; Conserv

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Score 480; DB 12; Pred. No. 1.9e-129; 0; Mismatches 115;

67.2%;

Sequence 1479 BP;

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                                   The invention relates to a novel polypeptide construct comprising at least one CDR3 region comprising at least one mutation in a fully defin sequence of 6 amino acids. A construct of the invention has antiinflammatory, antimicrobial, cytostatic, immunomodulator, and immunosuppressive activity. The polypeptide construct, polynucleotide, vector or composition are useful for the prevention, treatment or vector or composition are useful for the prevention, treatment or inflammatory disease, an immunological disease, an autoimmune disease an infectious disease in a human subject. The present sequence encodes bispecific single chain antibody scFv EpCAMxCD3 with the M69 mutant
                                                                                                                                                                                        Claim 22;
                                                                                                                                                                                                                  diseases comprises at least one mutated
                                                                                                                                                                                                                              Antibody construct, useful in treating,
                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                   Lanzavecchia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic. Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator; immunosuppressive; proliferative disease; tumour; inflammatory disease; immunological diseavder; autoimmune disease; infectious disease; scrv EpCAMxCD3; antibody; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody scrv EpCAMxCD3 with
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                          in the
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                                                                                                                                                                                        SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                 2002CA-02403313
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                          anti CD3 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "scFv EpCAMxCD3 with M69 mutant in anti CD3
region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "No start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_except= (pos:1054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .1479
                                                                                                                                                                                        86; 80pp; English.
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CDR3 region.
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Bisp
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CDR3
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  Query Match 67.
Best Local Similarity 81.
Matches 587; Conservative
                                                                                                                                                      The invention relates to a novel polypeptide construct comprising at least one CDR3 region comprising at least one mutation in a fully defined sequence of 6 mino acids. A construct of the invention has antiinflammatory, antimicrobial, cytostatic, immunomobulator, and immunosuppressive activity. The polypeptide construct, polynucleotide, vector or composition are useful for the prevention, treatment or amelioration of a proliferative disease, a tumorous disease, an inflammatory disease, an immunological disorder, an autoimmune disease or an infectious disease, an immunological disorder, an autoimmune disease or an infectious disease in a human subject. The present sequence encodes bispecific single chain antibody scfv EpCAMXCD3 with the M13 mutant peptide in the anti CD3 region.
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/note= "No start codon"
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2002; 2002CA-02403313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bispecific single chain antibody scFv EpCAMxCD3 with the M31 mutant peptide in the anti CD3 region.
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DB; ADS99445.
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                                                                                                     ATCGCAGGTGCAGGTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTC
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GCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGTGGAAGCACAAATTA
                                                      CATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGGTGTACACTGGGTTCGCCA
                                                                                     TTCTCAGGTGAAACTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTC
                                                                                                                                            AGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCT------
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                                                                                                                                                                                                                                                                           CTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCTGA 242
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                            CATCACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCGCCA
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D; Mismatches 115;
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                 The invention relates to a novel polypeptide construct comprising at least one CDR3 region comprising at least one mutation in a fully defir sequence of 6 amino acids. A construct of the invention has antiinflammatory, antimicrobial, cytostatic, immunomodulator, and immunosuppressive activity. The polypeptide construct, polynucleotide, vector or composition are useful for the prevention, treatment or amelioration of a proliferative disease, a tumorous disease, an inflammatory disease, an immunological disorder, an autoimmune disease an infectious disease in a human subject. The present sequence encodes bispecific single chain antibody scFv EpCAMxCD3 with the M9 mutant poptide in the anti CD3 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDR3; antiinflammatory; antimicrobial; cytostatic; immunosuppressive; proliferative disease; tumour; immunological disorder; autoimmune disease; infecti
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Pred. No. 1.9e-129;
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0; Mismatches 1
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least one CDR3 region comprising at least one mutation in a fully defi sequence of 6 amino acide. A construct of the invention has antiinflammatory, antimicrobial, cytostatic, immunomodulator, and immunosuppressive activity. The polypeptide construct, polynucleotide, vector or composition are useful for the prevention, treatment or amelioration of a proliferative disease, a tumorous discourse.
                                                                                                                                                                                                Claim
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory disease, an immunological disorder, an autoimmune an infectious disease in a human subject. The present sequence bispecific single chain antibody scFv EpCAMXCD3 with the M4 mut peptide in the anti CD3 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1479 BP;
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                   GGGTAACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTC
                                                 CTTTAAAATGAACAGTCTGCAAGCTAATGACACAGCCATATATTACTGTGCCAGAATGG-
                                                                  CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTGCCAGTCGGGG
                                                                                                       TAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAAGTTTT
                                                                                                                                 TAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTT
                                                                                                                                                                                      GCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGTGGAAGCACAAATTA
                                                                                                                                                                                                                  CATCACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTTCGCCA
                                                                                                                                                                                                                                          CATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGGTGTACACTGGGTTCGCCA
                                                                                                                                                                                                                                                                       TTCTCAGGTGAAACTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTC
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-AGAACTGGTCGTTTGCTTACTGGGGGCCAAGGGACCACGGTCACCGTCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 A; 364 C;
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                                                                                                                                                            rctggagtggctgagtgatatggagtggtaggaagcacagacta
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No. 1.
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.9e-129;
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ADS99442 standard; DNA; 1479 ₽P

(first entry)

Antibody 8CF'V EpcAMxcD3 with M14 mutant in anti CD3 region

RESULT 13
ADS99442
ID ADS99
XX ADS99
XC ADS99
XX DE O2-DE
XX V2-DE
XX CDR3;
XW immur
KW immur CDR3; antiinflammatory; antimicrobial; cytostatic immunosuppressive; proliferative disease; tumour; immunological disorder; autoimmune disease; infec cytostatic; infectious inflammatory immunomodulator; disease;

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Best Local S
Matches 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel polypeptide construct comprising at least one CDR3 region comprising at least one mutation in a fully defin sequence of 6 amino acids. A construct of the invention has antiinflammatory, antimicrobial, cytostatic, immunomodulator, and immunosuppressive activity. The polypeptide construct, polynucleotide, vector or composition are useful for the prevention, treatment or amelioration of a proliferative disease, a tumorous disease, an inflammatory disease, an immunological disorder, an autoimmune disease an infectious disease in a human subject. The present sequence encodes bispecific single chain antibody scFv EpCAMxCD3 with the M14 mutant peptide in the anti CD3 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody
diseases
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Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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587; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   construct, useful in treating, e.g., comprises at least one mutated CDR3
                                                                                                                                                          CTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCTGA
                                                                                                                                                                                                                                  GCAGTCTCCGAAACTGCTGATATACTCTGCATCCAATCGCTACACTGGAGTCCCCTGATCG
                                                                                                                                                                                                                                                                             CACCTGCAAGGCCAGTCAGAATGTGGGTACTAATGTAGCCTGGTATCAACAGAAACCAGG
                                                                                                                                                                                                                                                                                                  AACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTGGCTTGGTACCAACAGAAGCCAGG
                                                                                                                                                                                                                                                                                                                                                                              TATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1479
                   GACCAAGCTGGAAATAAAAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGG
                                                                                         AGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCT-----CGCTCGGAGGGGGG
                                                                                                                                                                                                            GCAATCTCCTAAAGCACTGATTTACTCGGCATCCTACCGGTACAGTGGAGTCCCTGATCG
                                                                                                                                                                                                                                                                                                                                                   TATCCAGCTGACCCAGTCTCAAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGT
 CTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATGTGCAGTCTGA
                                                                      AGACTTGGCAGAGTATTTCTGTCAGCAATATAACAGCTATCCGCTCACGTTCGGTGCTGG
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llarity 81.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 385 A; 364 C;
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/note= "No start codon"
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/product= "scFv EpCAMxCD3
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 480; DB 13;
Pred. No. 1.9e-129;
0; Mismatches 115;
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defined
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RESULT 14
ADS99432
ID ADS99
XX ADS99
XX ADS99
XX ADS99
XX CDR3
XX CDR3
XX CDR3
XX Inmn
XX Inmn
XX Inmn
XX Inmn
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XX Inmn
XX ET CDE
FT CD
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   The invention relates least one CDR3 region
                                                                                                                                          WPI; 2004-390792/37.
P-PSDB; ADS99431.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
Unidentified.
                                                     Claim
                                                                                                                                                                                          Lanzavecchia
                                                                                                                                                                                                                            (MICR-) MICROMET
                                                                                                                                                                                                                                                                                               11-OCT-2002;
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                                                     ID NO
 region
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to a novel polypeptide construct comprising at least one mutation
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CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodula immunosuppressive; proliferative disease; tumour; inflammatory immunological disorder; autoimmune disease; infectious disease; scFv EpCAMxCD3; antibody; ds.
                                        Antibody construct, useful in treating, diseases comprises at least one mutated
                                                                                                                                                                                                                                                   11-OCT-2002; 2002CA-02403313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody scFv EpCAMxCD3 with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADS99432 standard; DNA; 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 ATCGCAGGTGCAGGTGAAGGAGTCAGGACCTTGGCCTGGTGGCGCCCTCACAGAGCCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGTGGAAGCACAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGGTGTACACTGGGTTCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCTCAGGTGAAACTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGTAACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTC
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/product= "scFv |
region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     note= "No start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAACTGGTCGTTTGCTTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTC
66; 80pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M7 mutant
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  English
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                                        region.
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inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutant
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                                                                and
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comprising in a fully

defined

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RESULT 15
ADS99444
ID ADS99
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DT 02-DE
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence of 6 amino acids. A construct of the invention has antiinflammatory, antimicrobial, cytostatic, immunomodulator, and immunosuppressive activity. The polypeptide construct, polynucleotide, vector or composition are useful for the prevention, treatment or amelioration of a proliferative disease, a tumorous disease, an inflatious disease, an immunological disorder, an autoimmune disease an inflectious disease in a human subject. The present sequence encodes bispecific single chain antibody scFv EpCAMxCD3 with the M7 mutant peptide in the anti CD3 region.
             02-DEC-2004
                                    ADS99444;
                                                           ADS99444
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587; Conserv
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                                                                                                                                                                                   CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTGCTACTGTGCCAGTCGGGG
                                                                                                                                                                                                                                                                  GTCTCCAGGAAAGGGTCTGGAGTGGCAGTGATATGGAGTGGTGGAAGCACAGACTA
                                                                                                                                                                                                                                                                                   GCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGGTTGGAAGCACAAATTA
                                                                                                                                                                                                                                                                                                                   CATCACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCGCCA
                                                                                                                                                                                                                                                                                                                                                                   TTCTCAGGTGAAACTGCAGGAGTCAGGACCTGGCCTAGTGCAGGCCCTCACAGAGCCTGTC
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                                                            standard;
                                                                                                                                             GGGTAACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTC
                                                                                                                                                                                                                     TAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAAGTTTT
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nilarity 81.5%;
Conservative
            (first
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                                                                                                                      AGAACTGGTCGTTTGCTTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTC
                                                           DNA;
            entry)
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                                                           1479
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Pred. No. 1.9e-
0; Mismatches
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l.9e-129;
les 115;
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Matches 587
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Unidentified
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CDR3; antiinflammatory; antimicrobi immunosuppressive; proliferative di immunological disorder; autoimmune
                                                                                Antibody scrv EpCAMxCD3
    antimicrobial; cytostatic; immunomodulator;
iferative disease; tumour; inflammatory disease;
autoimmune disease; infectious disease;
                                                                                    with M20
                                                                                    mutant
                                                                                    Ħ
                                                                                    anti
                                                                                    G
                                                                                  region
                                                                                encoding
                                                                                    DNA.
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antibody; ds.

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region"
/note= "No start codon"
                       /*tag= a
/product= "scFv EpCAMxCD3
                                                Location/Qualifiers
1. .1479
                         with
                        M20 mutant
                        in
                         anti
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11-OCT-2002; 2002CA-02403313

11-OCT-2002; 2002CA-02403313.

2004-390792/37. DB; ADS99443.

Antibody construct, useful in treating, diseases comprises at least one mutated e.g., cancer CDR3 region. and inflammatory

SEQ ID NO 78; 80pp; English.

The invention relates to a novel polypeptide construct comprising at least one CDR3 region comprising at least one mutation in a fully defin sequence of 6 amino acids. A construct of the invention has antiinflammatory, antimicrobial, cytostatic, immunomodulator, and immunosuppressive activity. The polypeptide construct, polynucleotide, vector or composition are useful for the prevention, treatment or amelioration of a proliferative disease, a tumorous disease, an inflammatory disease, an immunological disorder, an autoimmune disease an infectious disease in a human subject. The present sequence encodes bispecific single chain antibody scFv EpCAMxCD3 with the M20 mutant ij the anti CD3 region. at defined õ

Sequence 1479 BP; 385 A; 366 C; 389 ç 339 T; 0 U; 0 Other;

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Local Sinhes 587;
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
AGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCT------
                                                                                CTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCTGA
                                                                                                                                                           GCAGTCTCCGAAACTGCTGATATACTCTGCATCCAATCGCTACACTGGAGTCCCTGATCG
                                                                                                                                                                                                              CACCTGCAAGGCCAGTCAGAATGTGGGTACTAATGTAGCCTGGTATCAACAGAAACCAGG
                                                                                                                                                                                                                                        AACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTGGCTTGGTACCAACAGAAGCCAGG
                                                                                                                                                                                                                                                                                         TATCCAGCTGACCCAGTCTCAAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGT
                                                                                                                                                                                                                                                                                                                         TATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACCAT
                                                           CTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATGTGCAGTCTGA
                                                                                                                                   GCAATCTCCTAAAGCACTGATTTACTCGGCATCCTACCGGTACAGTGGAGTCCCTGATCG
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                              67.2%;
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                                                                                                                                                                                                                                                                                                                                                                Score 480; DB 13;
Pred. No. 1.9e-129;
0; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                   Length 1479;
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CGCTCGGAGGGGG
                                                                                                                                                                                                                                                                                                                                                                  18;
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                                                                                                                                     182
                       293
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•	662	654	603	594	543	534	483	474	423	414	363	354	303	294	243
	AGAACTGGTCGTTTGCTTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTC 713	GGGTAACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTC 713	CTTTAAAATGAACAGTCTGCAAGCTAATGACACAGCCATATATTACTGTGCCAGAATGG- 661	CTTAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTGCCAGTCGGGG 653	TAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAAGTTTT 602	TÄATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTT 593	GTCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGTGGAGGCACAGACTA 542	GCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGTGGAAGCACAAATTA 533	CATCACCTGCACAGTCTCGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCGCCA 482	CATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGGTGTACACTGGGTTCGCCA 473	TTCTCAGGTGAAACTGCAGGAGTCAGGACCTGGCCTAGTGCAGGCCCTCACAGAGCCCTGTC 422	ATCGCAGGTGCAGGTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTC 413	GACCAAGCTCGAGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGTG	GACCAAGCTGGAAATAAAAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGG 353	AGACTTGGCAGAGTATTTCTGTCAGCAATATAACAGCTATCCGCTCACGTTCGGTGCTGG 302

Search completed: February 18, 2005, 20:38:23 Job time : 422.122 secs

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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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; OTHER INFORMATION: 3G6-scFv-streptavidin US-09-142-974B-4
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US-09-142-974B-4
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Best Local Similarity
Matches 714; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA 'ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                             ATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTGGCTTGGTACCAACAGAAGCCA
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                                                                                                                                                                                                                  Score 714; DB 3;
Pred. No. 1.5e-208;
Mismatches 0;
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SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,416
FILING DATE: 27-00V-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/007,755
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fell, Perry
APPLICANT: Wittler, Robert
APPLICANT: Wittler, Gosta
TITLE OF INVENTION: MODIFIED SFV MOLECULES WHICH
TITLE OF INVENTION: MEDIATE ADHESION BETWEEN CELLS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE STORM
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version
                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica,
CITY: Los Angeles
STATE: CA
                                                                                                                                                                                                                                                           COUNTRY: 900
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                                                                                                                                                                                                                                                                                   USA
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TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other
US-08-756-416-31
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 752 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 30-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 3043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 310-445-9031
TELEX:
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                                                                                                                                                                                                                                                               GGAAGCACAAATTATAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACAACTCC
                                                                                                                                                                                                                                                                                                                                               CACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGT 519
                                                                                                                                                                                                                                                                                                                                                                                                                                TCACAGAGCCTGTCCATCACTTGCACTGGCTCTCGGGTTTTCATTAACCAATTATGGTGTA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCGGTGGAGGCACCAAGCTGGAAATCAAACGGGGTGGCGGTGGCTCGGGCGGTGGT
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                                                                                                           TGTGCCAGTCGGGGGGTAACTAC-----GGCTATGCTTTGGACTACTGGGGTCAAGGA 693
                                                                                                                                                                                                                                            GGAAGCACAGACTATAATTCAGCTCTCAAATCCAGACTGAGCATCACCAAGGACAACTCC
                                                                                                                                                                                                                                                                                                                       AACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAATGATATGGGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                   TCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTCTCATTAACCGGCTATGGTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGGAGGAGGATGATATTGCAATGTATTTCTGTCAGCAAAGTAGGAAGGTTCCTTGGACG
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                                           ACCTCAGTCACCGTCTCCTC 713
                                                                                TGTGCCAGAGATGGTTATAGTAACTTTCATTACTATGTTATGGACTACTGGGGTCAAGGA
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76.9%;
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Pred. No. 8.8e-117;
0; Mismatches 141;
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CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/007,755

FILING DATE: 30-NOV-1995

ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B

REGISTRATION NUMBER: 34,470

REFERENCE/DOCKET NUMBER: 30436.

TELECOMMUNICATION:
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; Patent No. 6699715
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US-08-756-416-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1509 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 569; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT: Hayden, Martha
APPLICANT: Fell, Perry
APPLICANT: Mittler, Robert
APPLICANT: Witberg, Gosta
TITLE OF INVENTION: MODIFIED SFV MOLECULES WHICH
TITLE OF INVENTION: MEDIATE ADHESION BETWEEN CELLS
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/756,416
FILING DATE: 27-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 11150 Sant:
CITY: Los Angeles
STATE: CA
COUNTRY: USA
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                                                                                                                                                                                                                                                             64 ACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTGGCT-----TGGTACCAA 111
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  GTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGC--
                                                                        GTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACCTTTCACCATCAGCACT
                                                                                                                                CAGAAACCAGGACAGCCACCCAAACTCCTCATCTCTGCATCCAACGTAGAATCTGGG 180
                                                                                                                                                              CAGAAGCCAGGGCAGTCTCCGAAACTGCTGATATACTCTGCATCCAATCGCTACACTGGA 171
                                                                                                                                                                                                                    TCCTGCAGAGCCAGTGAAAGTGTTGAATATTATGTCACAAGTTTAATGCAGTGGTACCAA
                                             ATTGTGCTCACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGTCAGAGAGCCACCATC
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                                                                                                                                                                                                                                                                                                                                                                                         58.0%; Score 414.4; DB 4; 76.9%; Pred. No. 1.2e-116; tive 0; Mismatches 141;
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                                          240
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APPLICANT: Hayden, ....
APPLICANT: Fell, Perry
APPLICANT: wittler, Robert
APPLICANT: wittler, Robert
APPLICANT: Winberg, Gosta
TITLE OF INVENTION: MCDIATE
TITLE OF INVENTION: MEDIATE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
Annressse: Merchant & Go
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US-08-756-416-29
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                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/756,416
FILING DATE: 27-NOV-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/007,755
FILING DATE: 30-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B
REGISTRATION NUMBER: 34,470
                                                                                                                                             ZIF: 90025

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASKERO Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                     STREET: 11150 Santa Monica, Suite CITY: Los Angeles
STATE: CA
COUNTRY: 'USA
ZIP: quare
REFERENCE/DOCKET NUMBER: 30,470
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US-08-756-416-29
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SEQUENCE CHARACTERISTICS:
LENGTH: 1527 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Other
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Pred. No. 1.2e-116;
0; Mismatches 141;
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NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATE;
APPLICATION NUMBER: US,
FILING DATE: 1-APR-1993
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APPLICATION NUMBER: 512,910
FILING DATE: 25-APR-1990
APPLICATION NUMBER: 299,617
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 92,110
FILING DATE: 02-SEP-1987
APPLICATION NUMBER: 902,971
APPLICATION NUMBER: 902,971
APPLICATION NUMBER: 902,971
FILING DATE: 01-SEP-1986
EQ ID NO:16: 1
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                                         GAACGAATCTTTTACTATGCTATGGACTATTGGGGTCAAGGAACCTCAGTCACCGTCTCC
                                                              GGGGGTAACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC
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                                                                                                                 TTAAAAATGAACAGTCTGCAAATTGATGACACAGCCATATACTACTGTGCCAAACGACTG
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Pred. No. 6.9e-115;
0; Mismatches 163;
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APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN,
TITLE OF INVENTION: IMMUNOTHERAPHY USING SINGLE CHAIN
POLYPEPTIDE BINDING MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 57.2%;
Best Local Similarity 75.8%;
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PRIOR APPLICATION DATA:
APPLICATION UNUBER: 512,910
FILING DATE: 25-APR-1990
APPLICATION NUMBER: 299,617
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 92,110
FILING DATE: 02-SEP-1987
APPLICATION NUMBER: 902,971
APPLICATION NUMBER: 902,971
APPLICATION NUMBER: 902,971
FILING DATE: 01-SEP-1986
3Q ID NO:16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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TTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTGCCA---GTCGG
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                                                                                  AATTCOGCTCTTATGTCCAGACTGAGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTTC
                                                                                                                                                                                                                                  ATCACTIGCACIGICTCTGGGTTTTCATTAACCAATTATGGTGTACACTGGGTTCGCCAG
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                                                                                                                                     CCTCCAGGAAAGGGTCTGGAGTGGCTGGAGTAATATGGGCTGGTGGAAACACAAATTAT
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                                                            AGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAATTCCAAGAGCCAAGTTTTC
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Pred. No. 6.9e-115;
0; Mismatches 163;
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RESULT 8
US-08-756-416-38
                                                                                                                                                                                                             ; FEATURE:
US-08-756-416-38
                                                                                                                                              Matches
                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/756,416
FILING DATE: 27-NOV-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/007,755
FILING DATE: 30-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 824 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT: Winberg, Gosta
TITLE OF INVENTION: MODIFIE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESO VERSION 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 310-445-1140
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                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                TOPOLOGY:
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REFERENCE/DOCKET NUMBER: 30436.41US01
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Adriano, Sarah B
REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 11150 San
CITY: Los Angeles
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 310-445-9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Merchant & Gould STREET: 11150 Santa Monica,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    667
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     TCCTGCAGAGCCAGTGAGAGTGTTGAATATTATGTCACAAGTTTAATGCAGTGGTACCAG 189
                            ACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTGGCT-----TGGTACCAA 111
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                                                                        ATTGTGCTCACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGAGCCACCATC 129
                                                                                                         ATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACCATA
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Fell, Pe
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                                                                                                                                          Conservative
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76.4%;
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                                                                                                                                          <u>,</u>
                                                                                                                                       Score 400.2; DB 4;
Pred. No. 2.1e-112;
0; Mismatches 138;
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                                                                                                                                                                                                                                                       Sequence 1, Application US/08860174A
Patent No. 5989830
GENERAL INFORMATION:
APPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOGT, Cornelis |
APPLICANT: VERHOEIJEN, Martine Eli
APPLICANT: WILSON, Stee
TITLE OF INVENTION: A BIFUNCTIONAL
TITLE OF INVENTION: ANTIBODY FRAGM
NUMBER OF SEQUENCES: 31
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ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE; Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS I
SOFTWARE: MS WORD, WINDOWS 95, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,1747
                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                      ADDRESSEE: PILLSBURY, MADISON STREET: 1100 New York Avenue, 1 STREET: 9th Floor, East Tower CITY: WASHINGTON 7
                                                                                                                                   COUNTRY: UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610
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     US/08/860,174A
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                                   Ver.
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; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 380..727
; OTHER INFORMATION: /pi
US-08-860-174A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: August 14, 1996 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 737 base pairs
TYPE: nucleic acid
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DESCRIPTION: 1
IMMEDIATE SOURCE:
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PRIOR APPLICATION UNDER: E
PPLICATION UNDER: E
PILING DATE: October:
APPLICATION UNDER: PI
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LOCATION: 335..379
OTHER INFORMATION:
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LOCATION: 11..730
OTHER INFORMATION:
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CAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGTGGAAGCACAAAT 531
                                                                                                                                   GGATCGCAGGTGCAGGTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTG
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                                                                                                                                                                             ACCAAGCTCGAGATCAAACGGGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTGGCTTGGTACCAACAGAAGCCAGGG 123
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                                                                                TCCATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGGTGTACACTGGGTTCGC
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/desc = "cDNA of
linker(s)"
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WMBER: PCT/EP/96/03605
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75.2%;
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Pred. No. 8e-112;
0; Mismatches 158;
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US-09-171-025-23;
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GENERAL INFORMATION:
APPLICANT:
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                                                                                                     Query Match
Best Local (
                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 737 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                               FEATURE: mat_peptide
NAME/KEY: mat_peptide
LOCATION: 380..727
OTHER INFORMATION: /product= "VHlys"
                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE: CLONE: ECORI-HindIII insert of pUR4124
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DESCRIPTION:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 11..730
OTHER INFORMATION:
                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                         NAME/KEY: misc_RNA
LOCATION: 335..379
                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
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                             14
                                                                                       Similarity 75.2
44; Conservative
ACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTGGCTTGGTACCAACAGAAGCCAGGG 123
                             ATCGAGCTCACCCAGTCTCCAGCCTCCCTTTCTGCGTCTGTGGGAGAAACTGTCACCATC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCA
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                                                          ATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACCATA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGGTAACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double
                                                                                                    55.8%;
75.2%;
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                                                                                                                                                                                                                           /product=
                                                                                                                                                                                                                                                                                     /product=
                                                                                                                                                                                                                                                                                                                                               /product= "VLlys-GS-VHlys"
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                                                                                      Score 398.2; DB 3;
pred. No. 8e-112;
0; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                  acid domains with synthetic linker(s)"
                                                                                                                                                                                                                           "(Gly4Ser)3 linker"
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RESULT 11
US-08-197-834-6
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APPLICANT: SHIMANURA, TOSHIRC
APPLICANT: SHIMANURA, HARUMI
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: IMUNOSUF
NUMBER OF SEQUENCES: TO
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application Patent No. 5639455
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,834
                                                                                                                                                                                              ADDRESSEE: P.C. STREET: 1755 S. CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                               ZIP: 22202
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134
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; LOCATION:
US-08-197-834-6
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NAME: Oblon, No. 5639455man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-661-0
TELEPHONE: (703) 413-3000
TELEPAX: (703) 413-220
TELEPAX: (703) 413-220
TELEPAX: 248855 OPAT UR
TELEX: 248855 OPAT UR
INFORMATION FOR SED ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
cmpa.morphures: aindia
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TOPOLOGY: linear
MOLECULE TYPE: Other
DESCRIPTION: DNA
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 0
FILING DATE: 17-FEB-1993
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       GTATTCCTCAAGATCACCAGTGTGGACACTGCAGATACTGCCACATACTTCTGTGCTCGA
                                                                                                                                                                                                 CGTCAGCCTTCAGGGAAGGGTCTGGAGTGGCTGGCACACATTTATTGGGATGATGACAAA
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1..738
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Pred. No. 3.3e-111;
0; Mismatches 153;
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RESULT 12 US-09-742-693-29

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APPLICANT: HOWELL, Steven
APPLICANT: LITTLE, Julie C.
APPLICANT: LAY DER LOGT, Cornelis P.
APPLICANT: PAN DER LOGT, Cornelis P.
APPLICANT: PAN DER LOGT,
TIFLE OF INVENTION: METHOD OF TREATING FABRICS
FILE REFERENCE: C7536 (V)
CURRENT APPLICATION NUMBER: US/09/742,693
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: EP99310431.4
PRIOR FILING DATE: 1999-12-22
NUMBER OF SEG ID NOS: 34
SOFTWARE: PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH TO THE PAUGHTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29, Applicate Patent No. 6579842 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA 'ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAATCTCCTCAGCTCCTGGTCTATTATACAACAACCTTAGCAGATGGTGTGCCATCAAGG
CCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGTGGAAGCACAAATTAT
                                                                                                                                                                                                                                                                                                                            AAGCTGGAAATAAAA---GGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGA 354
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Pred. No. 8.8e-111;
0; Mismatches 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 550; Conserv
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APPLICATION NUMBER: 512,910
FILING DATE: 25-APR-1990
APPLICATION NUMBER: 299,617
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 92,110
FILING DATE: 02-SEP-1987
APPLICATION NUMBER: 902,971
APPLICATION NUMBER: 902,971
FILING DATE: 01-SEP-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 1-APR-1993
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                                 TCCATCACTTGCACTGTCTCTGGGTTTTTCATTAACCAATTATGGTGTACACTGGGTTCGC 471
                                                                                                                                        GGATCGCAGGTGCAGGTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTG
                                                                                                                                                                                                                                                                                                                            GAAGATGCTGCCACTTATTACTGCCAGCAGTACAGTGGTTACCCACTCACGTTCGGTGCT
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Pred. No. 2e-110;
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Query Match Best Local S Matches 540

FEATURE:

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RESULT 14
5455030-14
; Patent NO. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN,
; TITLE OF INVENTION: IMMUNOTHERAPHY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
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Best Local
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FILING DATE: 1-APR-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 512,910
FILING DATE: 25-APR-1990
APPLICATION NUMBER: 299,617
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 92,110
FILING DATE: 02-SEP-1987
APPLICATION NUMBER: 902,971
PILING DATE: 01-SEP-1986
                                                                                                                                                                                                                                                                                                                                                                                                                           ID NO:14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 720
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                                                                               GAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAG-----CTCGCTCGGAGGG 291
                                                                                                                                                                                               GGGCAGTCTCCGAAACTGCTGATATACTCTGCATCCAATCGCTACACTGGAGTCCCTGAT
                                                                                                                                                                                                                                                       ACCTGCAAGGCCAGTCAGAGTGTGAGT---AATGATGTGGCTTGGTACCAACAGAAGCCA
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GGGACCAAGCTTGAGCTGGAAGGTAAA-----TCTTCTGGTTCTGGTTCCGAA
                   GGGACCAAGCTGGAAATAAAAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGC
                                                      GAAGATGCTGCCACTTATTACTGCCAGCAGTACAGTGGTTACCCCACTCACGTTCGGTGCT
                                                                                                              CGCTTCAGTGGCGGTGGGGTCTGGGACCTCTTACTCTCACAATCAGCAGTGTGGAGGCT
                                                                                                                                        CGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCT
                                                                                                                                                                      GGTGCCTCCCCAAACTCTGGGTTTATGGCACATCCAACTTCGCTTCTGGAGTCCCTGCT
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Pred. No. 2e-110;
0; Mismatches 149;
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APPLICANT: Porter, Robert A
APPLICANT: Badley, Robert A
TITLE OF INVENTION: Electroactive Surfaces
FILE REFERENCE: IMIN.P-036
CURRENT APPLICATION NUMBER: US/09/554,765
CURRENT FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: PCT/GB98/03495
PRIOR FILING DATE: 1998-11-23
PRIOR FILING DATE: 1998-11-23
SEQ ID NOS: 15
SOFTWARE: Patentin version 3.2
SEQ ID NO 12
LENGTH: 739
TYPE: DNA
ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE: ; OTHER INFORMATION: bispecific scFv4155-HCV3 and HCV24 construct US-09-554-765-12
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US-09-554-765-12
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Matches
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Patent No. 6551495
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Best Local (
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539; Conserv
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  TTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCTGAA
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                                        TTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAACCTGAA
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Pred. No. 2.7e-110;
0; Mismatches 163;
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CA 724	74 GATTĀTAGGCTTĞĀČTĀČTĞĞĞĞCGĀĀĞĞCĀČCĀČĞĞTČĀČĞTČTČTCA leted: February 18, 2005, 23:56:50 151.69 secs	arch comp	Se Db
CA 714	5 GGTAACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA	655	ઠ
GA 673	4 TTANANATGNACAGTCTGCACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAG	614	멍
GG 654	5 TTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTGCCAGTCGGGGG	595	ş
TC 613	4 AATTCAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACCAACTCCAAGAGCCAAGTTTTC	554	밁
TC 594	AATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACAACTCCCAAGAGCCAAGTTTTC	535	ð
AT 553	4 CCTCCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTTGGGGTGATGGAAACACAGACTAT	494	밁
AT 534	5 CCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGTGGAAGCACAAATTAT	475	ş
AG 493	ATCACATGCACCGTCTCAGGGTTCTCATTAACCGGCTATGGTGTAAACTGGGTTCGCCAG	434	멍
AG 474	5 ATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGGTGTACACTGGGTTCGCCAG	415	ક
CC 433	4 TCGCAGGTGCAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCC	374	문
CC 414	5 TCGCAGGTGCAGGTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCC	, 355	ş
GA 373	AAGCTCGAGATCAAACGGGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGA	314	문
GA 354	AAGCTGGAAATAAAAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGA	, 298	S
CC 313	4 GATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCTCGGACGTTCGGTGGAACC	254	밁

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Tue Feb 22 13:21:06 2005

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

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16: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

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Sequence 4, Appli Sequence 2, Appli Sequence 4, Appli Sequence 60, Appl Sequence 62, Appl Sequence 64, Appl Sequence 66, Appl Sequence 68, Appl Sequence 70, Appl Sequence 72, Appl Sequence 72, Appl Sequence 74, Appl	Description

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ALIGNMENTS

OY 1 AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACC	Query Match 100.0%; Score 714; DB 8; Length Best Local Similarity 100.0%; Pred. No. 8.8e-216; Matches 714; Conservative 0; Mismatches 0; Indels	RESULT 1 US-08-940-544-4 VS-08-940-544-4 VS-08-940-544-4 ; Sequence 4, Application US/08940544B ; Publication No. US20020018783A1 ; GENERAL INFORMATION: APPLICANT: CADELAIN, MICHEL APPLICANT: CREUNG, NAI-KONG V. APPLICANT: GUO, HONG-FEN APPLICANT: GUO, HONG-FEN TITLE OF INVENTION: USES THEREOF FILE REFERENCE: MSK.P-035-US CURRENT APPLICATION NUMBER: US/08/940,544B CURRENT FILING DATE: 1997-09-30 EARLIER APPLICATION NUMBER: PCT/US97/04427 EARLIER FILING DATE: 1997-03-20 VUMBER OF SEQ ID NOS: 4 SOFTWARE: PATENTIN VET. 2.0 SEQ ID NO 4 LENGTH: 714 TYPE: DNA ORGANISM: HUMAN FEATURE: OTHER INFORMATION: 3G6-scFv US-08-940-544-4
AGCAGGAGAC AGCAGGAGAC	714;	N ANTIBODY
AGGGTTACO AGGGTTACO	0; Gaps	AND CD28
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CURRENT APPLICATION NUMBER: US/10/075,947A
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 09/142,974
PRIOR FILING DATE: 1998-09-18
PRIOR PELLING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/013,703
PRIOR FILING DATE: 1997-03-20
PRIOR APPLICATION NUMBER: 60/013,703
PRIOR APPLICATION NUMBER: 60/013,703
PRIOR FILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 714
TYPE: DNA
ORGANISM: Murine
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US-10-075-947A-2
Sequence 2, Application US/10075947A
; Dublication No. US20030147808A1
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APPLICANT: Rivlin, Ken
APPLICANT: Sadelain, Michel
TITLE OF INVENTION: Single Chain FV Constructs of
TITLE OF INVENTION: Antibodies
FILE REFERENCE: MSK. P-013-2
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cheung, Nai-Kong V
APPLICANT: Larson, Steven M.
APPLICANT: Guo, Hong-Fen
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Sequence 4, Application US/10075947A

Publication No. US20030147808A1

GENERAL INFORMATION:
APPLICANT: Cheung, Nai-Kong V.
APPLICANT: Larson, Steven M.
APPLICANT: Guo, Hong-Ten
APPLICANT: Sadelain, Michel
ITITLE OF INVENTION: Single Chain FV Constructs of
ITITLE OF INVENTION: Antibodies
FILE REFERENCE: MSK.P-013-2
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 09/142,974
PRIOR FILING DATE: 1998-09-18
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PRIOR APPLICATION NUMBER: PCT/US97/04427
PRIOR FILING DATE: 1997-03-20
PRIOR PILING DATE: 1996-03-20
NUMBER OF SEO ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 1173
TYPE: DNA
ORGANISM: Murine
FEATURE:
FEATURE: TIPOTHERING OF SECTION 1173
TYPE: DNA
ORGANISM: Murine
RESULT 4
US-10-682-845-60
(Sequence 60, Application US/10682845
Publication No. US20040162411A1
GENERAL INFORMATION:
APPLICANT: Lanzavecchia, Antonio
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Pred. No. 1.1e-215;
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Best Local Similarity
Matches 587; Conserv
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FITTLE OF INVENTION: Potent T cell modulating mol
FILE REFERENCE: G2296 US
CURRENT APPLICATION NUMBER: US/10/682,845
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR FILING DATE: 2002-10-11
PRIOR FILING DATE: 2002-10-11
PRIOR FILING DATE: 2002-10-11
PRIOR FILING DATE: 2002-10-11
SEQ ID NO 60
LENGTH: 1479
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
FEATURE:
OFFICE INDOMNATION: COR. FEATURE:
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                         GGGTAACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTC
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Pred. No. 2.1e-141;
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US-10-682-845-62
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TITLE OF INVENTION: POCENT T cell modulating
FILE REFERENCE: G2296 US
CURRENT APPLICATION NUMBER: US/10/682,845
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION UNMERS: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 89
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nt T cell modulating molecules
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Pred. No. 2.1e-141;
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US-10-682-845-64
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SEQ ID NO 64
LENGTH: 1479
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Best Local Similarity 81.5%;
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CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 89
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                    CTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTACTGTGCCAGTCGGGG
                                                                      TAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAAGTTTT
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Pred. No. 2.1e-141;
0; Mismatches 115;
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RESULT 7

US-10-682-845-66

Sequence 66, Application US/10682845

Publication No. US20040162411A1

GENERAL INFORMATION:
APPLICANT: Lanzawecchia, Antonio
ITILE OF INVENTION: Potent T cell modulating mol
FILE REFERENCE: G2296 US
CURRENT APPLICATION NUMBER: US/10/682,845

CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR TILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11

PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11

SEQ ID NO 66

SETWARE: Patentin version 3.1

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OTHER INFORMATION: SCFV EPCAMXCD3 with
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                  TAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTTT
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81.5%;
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Pred. No. 2.1e-141;
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ITITLE OF INVENTION: Potent T cell modulating mo:
FILE REFERENCE: G2296 US
CURRENT APPLICATION NUMBER: US/10/682,845
CURRENT APPLICATION NUMBER: US 60/419,149
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.1
SEQ ID NO 68
LENGTH: 1479
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
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US-10-682-845-68
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                 GCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGAGGGAAGCACAAATTA 533
                                                                                 CATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGGTGTACACTGGGTTCGCCA 473
                                                                                                                                               ATCGCAGGTGCAGGTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTC
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GACCAAGCTCGAGATCAAAGGTGGTGGTGGTTCTGGCGGCGGCGGCTCCGGTGGTGGT
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No. US20040162411A1
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Pred. No. 2.1e-141;
0; Mismatches 115;
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CURRENT APPLICATION NUMBER: US/10/682,845
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PATENTIN VEYBION 3.1
SEQ ID NO 70
LENGTH: 1479
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US-10-682-845-70
US-10-682-845-70
; Sequence 70, Application US/10682845
; Publication No. US20040162411A1
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                    CATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGGTGTACACTGGGTTCGCCA
                                                                                       ATCGCAGGTGCAGGTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCCTCACAGAGCCTGTC
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CATCACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCGCCA
                                                                     TTCTCAGGTGAAACTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTC
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Pred. No. 2.1e-141;
0; Mismatches 115;
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CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 72, Application US/10682845
Publication No. US20040162411A1
GENERAL INFORMATION:
APPLICANT: Lanzavecchia, Antonio
TITLE OF INVENTION: Potent T cell modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Sir
Matches 587;
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LENGTH: 1479
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OTHER INFORMATION: SCFV EPCAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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TTCTCAGGTGAAACTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTC
                                                                   GACCAAGCTGGAAATAAAAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGG
                                                                                                                                                             AGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCT------
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Pred. No. 2.1e-141;
0; Mismatches 115;
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Sequence 74, Application US/10682845

Publication No. US20040162411A1

GENERAL INFORMATION:
APPLICANT: Lanzavecchia, Antomio
TITLE OF INVENTION: Potent T cell modulating molecules
FILE REFERNCE: G2296 US
CURRENT APPLICATION NUMBER: US/10/682,845

CURRENT FILING DATE: 2003-10-10

PRIOR APPLICATION NUMBER: US 60/419,149

PRIOR APPLICATION NUMBER: CA 2,403,313

PRIOR APPLICATION NUMBER: CA 2,403,313

PRIOR FILING DATE: 2002-10-11

NUMBER OF SEQ ID NOS: 89

SOFTWARE: PatentIn version 3.1

SEQ ID NO 74

LENGTH: 1479
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                                                                                                                                                                                                                                                                                                 AACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTGGCTTGGTACCAACAGAAGCCAGG
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                                GACCAAGCTGGAAATAAAAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGG 353
                                                                                                                                     CTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATGTGCAGTCTGA
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                                                                  AGACTTGGCAGAGTATTTCTGTCAGCAATATAACAGCTATCCGCTCACGTTCGGTGCTGG
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larity 81.5%;
Conservative
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Pred. No. 2.1e-141;
0; Mismatches 115;
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TITLE OF INVENTION: Potent T cell modulating mo;
FILE REFERENCE: G2296 US;
CURRENT APPLICATION NUMBER: US/10/682,845;
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149;
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11
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US-10-682-845-76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 76
                                                                                                                                                                                                                                                                                                                                                Matches
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TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
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                                                                                     CTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCTGA
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                                                                                                                                       GCAATCTCCTAAAGCACTGATTTACTCGGCATCCTACCGGTACAGTGGAGTCCCTGATCG
                                                                                                                                                                                                          CACCTGCAAGGCCAGTCAGAATGTGGGTACTAATGTAGCCTGGTATCAACAGAAAACCAGG
                                                                                                                                                                                                                                                                           TATCCAGCTGACCCAGTCTCAAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGT
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Pred. No. 2.1e-141;
0; Mismatches 115;
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RESULT 13

US-10-682-845-78

Sequence 78, Application US/10682845

Publication No. US20040162411A1

GENERAL INFORMATION:

APPLICANT: Lahzavecchia, Antonio

TITLE OF INVENTION: Potent T cell modulating mol

FILE REFERENCE: G2296 US

CURRENT APPLICATION NUMBER: US/10/682,845

CURRENT FILING DATE: 2003-10-10

PRIOR APPLICATION NUMBER: US 60/419,149

PRIOR APPLICATION NUMBER: CA 2,403,313

PRIOR APPLICATION NUMBER: CA 2,403,313

PRIOR FILING DATE: 2002-10-11

VOMBER OF SEQ ID NOS: 89

SOFTWARE: PatentIn version 3.1

SEQ ID NO 78

LENGTH: 1479
                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: scFv EpCAMxCD3 with M20 mutant in anti-CD3 part US-10-682-845-78
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Best Local S
Matches 587
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                                                                                                         GCAGTCTCCGAAACTGCTGATATACTCTGCATCCCAATCGCTACACTGGAGTCCCTGATCG
                           CTTCACTGGCAGTGGATATGGGACGGATTTCACCTTTCACCAGCACTGTGCAGGCTGA
                                                                        GCAATCTCCTAAAGCACTGATTTACTCGGCATCCTACCGGTACAGTGGAGTCCCTGATCG
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 CTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATGTGCAGTCTGA
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81.5%;
                                                                                                                                                                                                                                                                                                    Score 480; DB 18;
Pred. No. 2.1e-141;
0; Mismatches 115;
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TITLE OF INVENTION: Potent T cell modulating mo;
FILE REFERENCE: G2296 US;
CURRENT APPLICATION NUMBER: US/10/682,845;
CURRENT FILING DATE: 2003-10-10;
PRIOR APPLICATION NUMBER: US 60/419,149;
PRIOR FILING DATE: 2002-10-18;
PRIOR APPLICATION NUMBER: CA 2,403,313;
PRIOR FILING DATE: 2002-10-11;
NUMBER OF SEQ ID NOS: 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 80, Application US/10682845 Publication No. US20040162411A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 80
LENGTH: 1479
TYPE: DNA
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                             Matches 587;
                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: SCFV
                                                                                                                                                                                                                                                                                                                                         ORGANISM: artificial sequence FEATURE:
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                     GCAGTCTCCGAAACTGCTGATATACTCTGCATCCAATCGCTACACTGGAGTCCCCTGATCG
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GCAATCTCCTAAAGCACTGATTTACTCGGCATCCTACCGGTACAGTGGAGTCCCTGATCG
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Pred. No. 2.1e-141;
0; Mismatches 115;
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CURRENT APPLICATION NUMBER: US/10/682,845

CURRENT FILING DATE: 2003-10-10

PRIOR APPLICATION NUMBER: US 60/419,149

PRIOR FILING DATE: 2002-10-18

PRIOR FILING DATE: 2002-10-11

NUMBER OF SEQ ID NOS: 89

SOFTWARE: Patentin version 3.1

SEQ ID NO 82

LENGTH: 1479

TYPE: DNA

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: SCFV EPCAMXCD3 with M58 mutant in anti-CD3 par'

US-10-682-845-82
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-682-845-82

| Sequence 82, Application US/10682845

| Publication No. US20040162411A1

| GENERAL INFORMATION:
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Best Local Similarity 81.5%;
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                                                          TATCCAGCTGACCCAGTCTCAAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGT
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                                                                                                               Score 480; DB 18; Length 1479;
Pred. No. 2.1e-141;
0; Mismatches 115; Indels 18
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ALIGNMENTS

REFERENCE AUTHORS TITLE SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 BI690298 LOCUS DEFINITION FEATURES COMMENT Bource DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11878 row: i column: 06 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey Green M.D. cDNA Library Preparation: Life Technologies, cDNA Library Arrayed by: The I.M.A.G.B. Consc 1 (bases 1 to 840) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Eukaryota; Metazoa; Mammalia; Eutheria; Mus musculus BI690298.1 GI:15652927 mRNA sequence. Mus musculus (house mouse) quality sequence stop: 828. Location/Qualifiers /mol type="mrNA" /strain="FVB/N" /db xref="taxon:10090" /db xref="taxon:10090" /clone="IMAGE:5345741" /sex="female, virgin" /tissue_type="infiltrating ductal carcinoma" /dev_stage="5 months" /lab host="DH10B" /clone_ilb="NCI_CGAP_Mam6" /clone_ilb="NCI_CGAP_Mam6" /clone_ilb="NCI_COned unddirectionally. Primer: Oligo dT. Site_2: Not; Cloned unddirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH" organism="Mus musculus" .840 Chordata; Rodentia; 840 bp Mus bp mRNA linear BST 18-SEP-2001 musculus cDNA clone IMAGE:5345741 5', Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus Consortium ag a Mus.

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BU522581.1 GI:22830107
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Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGTGCCAGTGGGGGTTACTAACGGAGGGTGCTATGGACTACTGGGGTCAAGGAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTGCCAGTCGGGGGGGTAACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTC
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                                                                                                                                                                                                                                                                                        quality sequence stop: 723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                           /clone="IMAGE:6529074"
/lab_host="HH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_CO24"
/clone_Torgan: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo d'Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
                                                                                                                                                                                             /mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                       _xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse)
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               440 bp mRNA linear EST 19-NOV-200 K0711B09-5N NIA Mouse Hematopoietic Stem Cell (Lin-/G-Kit-/Sca-1-) CDNA Library (Long) Mus musculus cDNA clone NIA:K0711B09 IMAGE:30074612 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                  Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Ca: Aiba,K., Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H. Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (Lin-/G-Kit-/Sca-1-) cDNA Library (Long) Unpublished (2001)
                                                                                                                                                                                                                                                                                                                        Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1. (bases 1 to 480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                            Seq primer: M13 Reverse
High quality sequence stop:
                                                                                                                                                                                                                                                                                    Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0711 row: B column: 09
                                                                                                                                                                                                                                                                                                                                                                                    Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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                                   /tissue_type="Hematopoietic Stem Cell
(Lin-/c-Kit-/Sca-1-)"
                                                                                                                                                                                                           Location/Qualifiers
/dev_stage="Age approx.10 weeks old"
/lab_host="DH10B"
                                                                           clone="NIA:K0711B09 IMAGE:30074612"
                                                                                           /mol_type="mRNA"
/strain="C57BL/6NCr"
/db_xref="niaEST:K0711B09-5N"
/db_xref="taxon:10090"
                                                                                                                                                                       organism="Mus musculus"
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Pred. No. 6.1e-72;
D; Mismatches 45
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                                               BF182141
BF182141.1
EST.
                                                                        BF182141
601804682F1 NCI_CGAP_Mam5
mRNA sequence.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                    Mus musculus (house mouse)
                                                                                                                                                                                             CAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTA 638
                                                                                                                                                                                                                                                                                                                                                                               CTCACAGAGCCTGTCCATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                       CTCTGGCGGTGGCGGATCGCAGGTGCAGGTGAAGGAGTCAGGACCTGGCCTGGTGGCGCC
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                                                                                                                                                                                                                                                                                                                                                                   CTCACAGAGCCTGTCCATCACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGT
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                                                                                                                                                                        TCAGTCACCGTCTCCTCA 714
                                                                                                                                                                                                                                       CAAGAGCCAAGTTTTCTTTAAAAATGAACAGTCTGCAAGCTGATGACACAGCCATATATTA
                                                                                                                                                                                                                                                                               TGGAAGCACAGACTATAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTC
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Pred. No. 1e-71;
0; Mismatches
                                                                                                  671 bp
                                                                                        Mus musculus cDNA
                                                                                                  mRNA
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A clone IMAGE:4035429 5',
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ACCESSION VERSION KEYWORDS

ORGANISM

RESULT 4 BF182141 LOCUS

DEFINITION

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VERSION
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AUTHORS
TITLE
JOURNAL
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                                 BE309592
601094848F1 NCI_CGAP_Mam5
mRNA_sequence.
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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NIH-MGC http://mgc.nci.nih.gov.
National Institutes of Health,
Unpublished (1999)
BE309592
BE309592.1
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall
Site_2: NotI; Cloned unidirectionally. Primer: Ōligo dn
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
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/dev_stage="7 months"
/lab_host="DH10B"
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/strain="mix FVB/N, C5
/db_xref="taxon:10090"
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 GI:9168025
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Pred. No. 1.7e-71;
0; Mismatches 61;
                                                         594 bp mRN
Mus musculus
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lth, Mammalian Gene Collection (MGC)
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IMAGE:3489635 5',
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KEYWORDS
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BF578188
602094691F1 NCI
mRNA sequence.
BF578188
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Mus musculus
Mus musculus
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1 (Dases 1 to 594)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                               GGGCAGTCTCCGAAACTGCTGATATACTCTGCATCCAATCGCTACACTGGAGTCCCTGAT
                                                                                                                                                                                                                                                   GAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCT------CGCTCGGAGGG 291
                                                                                                                                                                                                                                                                                                              CGCTTCACTGGCAGTGGATATGGGACGGATTTCACCTTTCACCATCAGCACTGTGCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTGGCTTGGTACCAACAGAAGCCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall
/site_2: NotI, Cloned unidirectionally. Primer: Oligo di
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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/clone="IMAGE:3489635"
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/strain="mix FVB/N, C57BL/6J"
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                              691 bp mRNA linear EST 12-DEC-2000 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4209022 5',
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Pred. No. 9.4e-71;
0; Mismatches 17;
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lead through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9774 row: e column: 23
High quality sequence stop: 690.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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EST.
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                         AGTCACCGTCTCCTCA
                                                                                        CTGTGCCA
                                                                                                                       CTGTGCCAGTCGGGGGGAACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTC
                                                                                                                                                                               CAAGAGTCAAGTTTTCTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCAGGTACTA
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/db xref="taxon:10090"
/clone="InARGE:4209022"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NCI_CGAP_CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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Pred. No. 2.5e-69;
0; Mismatches 45
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BQ940476 970 bp mRNA linear EST AGENCOURT_8879458 NCI_CGAP_Co24 Mus musculus cDNA clone

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BQ940476
BQ940476.1 GI:
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14015 row: C column: 21
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Mammalla; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 970)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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                                                                         CTGTGCCAGTCGGGG----GGGTAACTACGGCTATGGACTTGGGACTACTGGGGTCAAGGAAC
                                                                                                                             CAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCAAACTGATGACACAGCCATGTACTA 638
                                                                                                                                                                                       TGGAAGCACAAATTATAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACAACTC 578
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                                                                                                              CAAGAGCCAAGTCTTCTTAAAAATGAACAGTCTCCAAACTGATGACACAGCCATGTATTA
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                            CTCAGTCACCGTCTCCTCA 714
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:6475820"
/lab host="DH108 (1 phage-resistant)"
/clone_lib="NCI_CGAP_CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo d
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/mol_type="mRNA"
/strain="FVB/N"
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Pred. No. 3.5e
0; Mismatches
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                Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 930)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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1 (bases 1 to 831)
Adams,D.J., Biggs,P.J., Cox,A.V.,
Jonkers,J., Smith,J., Plumb,R.W.,
Rogers,J. and Bradley,A.
Direct Submission
                                                                                                                                                                                                                                                                                  602095631F1 NCI_CGAP_Co24 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (20-FEB-2004) Sanger Centre, Hinxton, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                        Mus musculus
                                                                                                                                                                        Mus musculus (house mouse)
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Similarity 91.4%;
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN40c19"
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Rodentia;
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Pred. No. 2.5e-65;
0; Mismatches 26;
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Mus musculus
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Taylor, R.G., Nishijima, I., Yu, Y.,
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IMAGE: 4215751 5',
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                                                                                                                                                     792 bp
AGENCOURT 28626487 NIH MGC 249 R
IMAGE:7379450 5', mRNA sequence.
CO567792
CO567792.1 GI:50380421
EST.
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
NIH-MGC
                                                                                                        Rattus norvegicus (Norway rat)
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                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAAGTGGCTGGGAGTAATATGGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGATTCTCATTAACCAGCTATGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCACAGAGCCTGTCCATCACTTGCACTGCTCTCTGGGTTTTCATTAACCAATTATGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCAAGCTGTGTCCTGTCCCAGGTGCAGCTGAAGGAGACAGGACCTGGCCTGGTGGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCTGGCGGTGGCGGATCGCAGGTGCAGGTGAAGGAGGTCAGGACCTGGCCTGGTGGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGAGCCAAGTTTTCTTAAAAATGAATAGTCTCCAAACTGATGACACAGCCATATACTA
                        (bases 1 to 792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 633.
Location/Qualifiers
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  http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxxn:10090"
/dloxref="taxxn:10090"
/clone="IMAGE:4215751"
/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP_C024"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: colon; Vector: pCMY-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       moi_type="mRNA
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.8%;
83.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 262.4; 1
Pred. No. 2.6e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>,,</u>
                                                                                                                                                                                                                                     Rattus norvegicus cDNA clone
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hes 61;
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                                                                                                                                                                                                                                                             linear
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                                                                                                                                                      386
446
                                                                       704
                                                                                                                                                                                                                                                                                                     326 ACCAAGTTTTCTTAAAAATGAACAGTCTGCAAACTGAAGACACAGCCATTTACTACTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 ÁGACCCTGTCCCTCACCTGCACTGTCTCTGGATTCTCATTAATGGACTACAGTGTACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 GCGGTGGCGGATCGCAGGTGCAGGTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCCTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301;
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High quality sequence stop: 703.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM15536 row: f column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard
College of Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Institutes of Health, Mammalian Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                               CCGTCTCCTCA 714
                                                                                                                                                                                                  CCAGTCGGGGGGTAACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCA
                                                                                                                                                                                                                                                                                                                                                    GCCAAGTTTTCTTAAAAATGAACAGTCTGCAAACTGATGACACACCCATGTACTACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACACATATTATAATTCAGCTCTCAAATCCCGACTGAGCATCAGCAGGGACACCTCCAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAGCCTGTCCATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGGTGTACACT
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CAGTCTCCTCA 456
                                                                                                                                                      CCAGAGCACCGGGATACAGTGGTGACTACTTTGATTACTGGGGCCAAGGAGTCATGGTCA
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/db xref="taxon:10116"
/db xref="taxon:10116"
/clone="IMGE:7379450"
/lab host="PHIOB TonA"
/lab host="HIOB TonA"
/clone="Ib="NIH_MGC_249"
/clone="Torgan: spleen; Vector: pExpress-1; Site_1: EcoRV;
/note="Torgan: spleen; Vector: pE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 259; DB 7;
Pred. No. 2.5e-64;
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AUTHORS
TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                    404
                                            524
                                                                                         214
                                                                                                                                        464
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                                                                                                                                                                                                                                                                                                                   344 GCGGTGGCGGATCGCAGGTGCAGGTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCCTCAC
                                                                                                                                                                                                                                                                                   94
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AGENCOURT 28451299 NIH MGC 248 Rattus norvegicus cDNA clone
IMAGE:7366659 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 46
High quality sequence stop: 699.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov b column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 2089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CO574382.1 GI:50387011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                    GGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGGTGGAA 523
                                                                                                                                                                                                                  AGAGCCTGTCCATCACTTGCACTGTCTCTGGGTTTTCATTAACCAATTATGGTGTACACT 463
                                                                                                                                                                                                                                                                                   GCTGTGTCCTGTCCCAGGTGCAGCTGAAGGAGCTCAGGACCTGGCCTTGTGCAGCCCTCAC 153
                                          GCACAAATTATAATTCGGCTCTTATGTCCAGACTGAGCATCAGCAAGGACAACTCCAAGA 583
                                                                                                                                                                                    AGACCCTGTCCCTCACCTGCACTGTCTCTGGGTTCTCATTAACCAGCTATAATGTACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 793)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B TonA"
/clone lib="NIH MGC 248"
/clone lib="NIH MGC 248"
/note="Organ: spleen; Vector: pExpress-1; Site_1: EcoRV;
/note="Organ: spleen; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (Tri-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGAGCGCCC(T)25-3' and cloned into
the EcoRV/Not! sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.7 kb. This is a
primary library (normalized library is NIH_MGC 249) and
was constructed by Open Biosytems. Note: this is a NIH_MGC
library"
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                     36.1%;
80.9%;
                                                                                                                                                                                                                                                                                                                                                                            Score 257.4; DB 7
Pred. No. 7.3e-64;
D; Mismatches 71
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                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7;
                                                                                                                                                                                                                                                                                                                                                                              71;
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                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                    213
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S

344 GCGGTGGCGGATCGCAGGTGCAGGTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCAC 403

Matches

305;

Conservative

<u>,</u>

Score 253; DB 7; Pred. No. 1.5e-62; 0; Mismatches 60

Length 914; Indels

6

Gaps

35.4%;

Query Match Best Local Similarity

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REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob,
College of Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLMM15523 row: p column: 11 High quality sequence start: 23 High quality sequence stop: 708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT 28542576 NIH MGC 248 Rattus
IMAGE: 3774685 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                                                                                  /lab_host="DH10B TonA"
/clone lib="NIH MGC 248"
/clone lib="NIH MGC 248"
/note="Torgan: spicen; Vector: pExpress-1; Site_1: EcoRV;
/note="Torgan: spicen; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (Tri-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T) 25-3' and cloned into
                                          the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb resulted in an average insert size of 1.7 kb. This is a primary library (normalized library is NIH MGC 249) and the constructed by Open Biosytems. Note: this Is a NIH_MGC via_constructed by Open Biosytems.
                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7374685"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 883)
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BF580610
BF580610.1 GI:11654322
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602093730F1 NCI_CGAP_Co24 Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus (house mouse)
                       Conservative
                                                                                                                      /clone="IMAGE:4208022"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                        db_xref="taxon:10090"
                                        35.1%;
                     Score 250.4; DB 2;
Pred. No. 8.4e-62;
0; Mismatches 21;
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musculus cDNA clone IMAGE:4208022 5',
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                                                                  305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.

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Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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AGENCOURT 10158089 NCI CGAP CO24 Mus
IMAGE:6529489 5', mRNA sequence.
RIK23804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 912)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM14129 row: 1 column: 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 653.
                                                                  Conservative
                                                                                                                                                               /clone="IMAGE:6529489"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dnaverage insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                        /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                          mol_type="mRNA"
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s musculus cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                             TITLE
                                                      Mammialia, Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammialia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (CE 1 (bases 1 to 664)

RS Okażaki, Y., Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikajdo, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schinbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Schinbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Grimmond, S., Hirokawa, N., Jackeon, I.J., Jarvis, E.D., Kanai, A., Kurochia, C., Codaik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackeon, I.J., Jarvis, E.D., Kanai, A., Kurochia, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, J.J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wang, L., Yang, I., Yang, L., Yang, L., Zavolan, M., Zhu, Y., Zimer, A., Carninci, P., Yang, L., Yang, L., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imcani, K., Ishii, Y., Ishino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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BY733751 RIKEN full-length enriched, adult male accessory axillary lymph node Mus musculus cDNA clone G630076H03 5', mRNA sequence.
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Contact: Yoshihide Hayashizaki
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Query Match
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639 CTGTGCCAGTCGGGGGGGTAACTACGGCTATG---
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="accessory axillary lymph node"
/dev stage="adult"
/clone_lib="RIKEN full-length enriched, adult
accessory axillary lymph node"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="G630076H03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 247; DB 6;
Pred. No. 7.7e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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